

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Edwards, Cynthia A.
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Andrews, Beth M.
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- (ii) TITLE OF INVENTION: Sequence-Directed DNA Binding
Molecules, Compositions and Methods
- (iii) NUMBER OF SEQUENCES: 664
- (iv) CORRESPONDENCE ADDRESS:
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 - (B) STREET: 505 Penobscot Drive
 - (C) CITY: Redwood City
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 94063
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/482,080
 - (B) FILING DATE: 07-JUN-1995
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/171,389
 - (B) FILING DATE: 20-DEC-1993
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/123,936
 - (B) FILING DATE: 17-SEP-1993
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/996,783
 - (B) FILING DATE: 23-DEC-1992
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/723,618
 - (B) FILING DATE: 27-JUN-1991
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/081,070
 - (B) FILING DATE: 22-JUN-1993
- (viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Brady, John F.
- (B) REGISTRATION NUMBER: 39,118
- (C) REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human ferredoxin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCTCTGCTTG CCAATGTCTT TATAGGTCAC CCGGAAGGCA CG

42

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human macrophage alphas-antitrypsin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCTACTGCCT CCACCCGAAG TCTACTTCCT GGGTGGGCAG GAAC

44

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene B for alpha 1-acid
glycoprotein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGTGACCGCC CATAGTTTAT TATAAAGGTG ACTGCACCCT GCAGCC

46

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene for alpha 1
microtubulin-bikunin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATTGGAGCTG TCCTTGGGGC TGTAATTGGC CCCAGCTGAG CAGGGCA

47

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene for alpha-2 macroglobulin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTGTTTGCAC ACAGAGCAGC ATAAAGCCCA GTTGCTTGG GAAGT

45

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human ACAA gene for peroxisomal 3-oxoacyl-CoA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CTCGGGTTTG GCTACAAAAG GTGGAAAGAC TTCCGGTCTG CATTCTG

48

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human ACAA gene for peroxisomal 3-oxoacyl-CoA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CAAGGTAGGC GGGGCATTGA GTGGAAAGCT CGGCTGGGCG GTGCCTGT

48

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human choline acetyltransferase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCAATTGTGA CCCACAGCCT AATAATAACA GTCTTTGCCC TCTTGCC

48

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human angiotensin I-converting enzyme gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGCGGGGGTG TGTCGGGTTT TATAACCCGC AGGGCGGCCG CGGCG

45

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human gene fragment for the acetylcholine receptor gamma

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGGGTGGGAG TGTAGGCTGT TATATGACAC CCAGAGCCCA TCTCT

45

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human cytokine (Act-2) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GTCCTAGGCC TCAGAGTCCC TATAAAGAGA GATTCCCAAC TCAGTA

46

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human beta-actin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12: .

GGTGAGTGAG CGGCGCGGGG CCAATCGCGT GCGCCGTTCC GAAAG

45

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human beta-actin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGCGGCCGC GCGGCGCCCC TATAAAACCC AGCGGCGCGA CGCGCCA

47

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

T E S T E R

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human cardiac actin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGCTCCAAC T GACCCTGTCC ATCAGCGTTC TATAAAGCGG CCCTCCTGGA

50

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene for vascular smooth
muscle alpha-actin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAGGAGAGCA GGCCAAGGGC TATATAACCC TTCAGCTTTC AGCTTCC

47

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human enteric smooth muscle
gamma-actin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AAGATCCGCC TCTGGGGTTT TATATTGCTC TGGTATTCAT GCCA

44

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human arachidonate 12-lipoxygenase
gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCGGGGCCGC AGACCGGTCC TTAAAGGTT GGAAGTGGCC CCGAGG

46

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human alcohol dehydrogenase alpha
subunit (ADH1) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGTGTTATTC AAGCAAAAAA AATAAATAAA TACCTATGCA ATACACCT

48

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human alcohol dehydrogenase beta
subunit gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GATGTTACAC AAGCAAACAA AATAAATATC TGTGCAATAT ATCTGCTT

48

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human alpha-fetoprotein gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TAACAGGCAT TGCCTGAAAA GAGTATAAAA GAATTTTCAGC ATGATTTTCC

50

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human cytosolic adenylate kinase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATGCCGCGCG CTGACAGCCT TATAAATAGT CGCCTTTGCC GGCCGCC

47

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human
alpha-N-acetylgalactosaminidase (AK1) gene

50

(D) TOPOLOGY: linear

46

(D) TOPOLOGY: linear

46

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human albumin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GAGAGTGACA AAGGCCTGAA TTTGTCAATT AGTAACAATT GTATTCAACA GTAAGGAT

58

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human aldolase A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CTGCTCACCA CACACAAGTG TTATAGGAGG AGTCTGGCCC TTGAG

45

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human aldolase C gene for fructose
1,6-bisphosphate aldolase

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ACCTGCAATA CCCCCTTACC CCAATACCAA GACCAACTGG CATAG

45

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human aldolase C gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGCATAGAGC CAACTGAGAT AAATGCTATT TAAATAAAGT GTATTTAATG AATTTCTCCA 60

AGCTTACGGA 70

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human aldolase A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CCTCCACACG TCAACGATTC TATTTGAAGT TGGGCAGGGG GTGGC 45

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human aldolase A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATTAGAGAAG ATCGGGGACA CATGTGGGGC TGGGCAGGAG CTG 43

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human aldolase A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GGGCTGGGCA GGAGCTGCCT TATAACCACC CGGGAACCCC TAGCT

45

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human aldolase A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GCGGAGGGCG GAGTGGTGCC TTAAAAGGC CGGCGCCGCC TTCCGC.

46

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human aldolase A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TGCGCCGCCC CTTCCGAGGC TAAATCGCTT CCTCTCGGAA CGCGC

45

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human aldolase B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AAAAAACATG ATGAGAAGTC TATAAAAATT GTGTGCTACC AAAGA

45

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human leukemia inhibitory factor
(LIF) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CTTACAACAC AGGCTCCAGT ATATAAATCA GGCAAATTCC CCATTGAGC

50

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human aminopeptidase N gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GGGGCTCCTC CCCTTTGGGG ATATAAGCCC GGCCTGGGGC TGCTCC

46

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human alpha-amylase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

AAATGTGCTT CTTACAGGAA TATAAATAGT TTCTGGAAAG GACACTG

47

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human amyloid-beta protein gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GGGAGGCCTG CGGGGTCGGA TGATTCAAGC TCACGGGGAC GAGCAGG

47

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human amyloid beta protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CGGGGACGAG CAGGAGCGCT CTCGACTTTT CTAGAGCCTC AGCGTCCTAG GACT

54

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human amyloid-beta protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GCGGGGTGGG CCGGATCAGC TGACTCGCCT GGCTCTGAGC CCCGCCG

47

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human amyloid-beta protein (APP)
gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TCAGCTGACT CGCCTGGCTC TGAGCCCCGC CGCCGCGCTC GGGCTCCGTC

50

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human pronatriodilatin precursor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TGCTTGAGG GCTGGGGGGC TATAAAAAGA GGCGGCACTG GGCAGC

46

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human gene for atrial natriuretic factor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TTGAAGTGGG AGCCTCTTGA GTCAAATCAG TAAGAATGCG GCTCTTGCA

49

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human gene for atrial natriuretic factor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CTGCGGATGA TAACTTTAAA AGGGCATCTC CTGCTGGCTT CTCACCTGG

49

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene for atrial natriuretic factor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TGCTTGGAGA GCTGGGGGGC TATAAAAAGA GCGGCACTG GGCAGC

46

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human atrial natriuretic factor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CTTGGAGAGC TGGGGGGCTA TAAAAAGAGG CGGCACTGGG CAGCTGGGAG

50

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human angiotensinogen gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CTCCATCCCC ACCCCTCAGC TATAAATAGG GCCTCGTGAC CCGGCC

46

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human heart/skeletal muscle ATP/ADP translocator gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

TCGCGAGAGC CCGGCGGGGA TATAAGGGGG AGCTGCGGGC CAGGC

45

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human apolipoprotein CIII gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TCTGGACACC CTGCCTCAGG CCCTCATCTC CACTGGTCAG CAGGTGACC

49

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human apolipoprotein CIII gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CTCAGGCCCT CATCTCCACT GGTCAGCAGG TGACCTTTGC CCAGCGCCC

49

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human apolipoprotein CIII gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TGCCTGCTGC CCTGGAGATG ATATAAAACA GGTCAGAACC CTCCTGCC

48

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human apolipoprotein CIII gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GACACCCTGC CTCAGGCCCT CATCTCCACT GGTCAGCAGG TGACCTTTGC

50

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human apolipoprotein CIII gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TGCCTGCTGC CCTGGAGATG ATATAAAACA GGTCAGAACC CTCCTGCC

48

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human apolipoprotein AII gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ATAATCCCTG CCCCACTGGG CCCATCCATA GTCCCTGTCA CCTGACAGG

49

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human apolipoprotein AII gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GGGGTGGGTA AACAGACAGG TATATAGCCC CTCCTCTCC AGCCAG

46

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human fetal gene for apolipoprotein
AI precursor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CTGCAGACAT AAATAGGCCC TGCAAGAGCT GGC

33

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human apolipoprotein B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GCCTGGGCTT CCTATAAATG GGGTGCGGGC GCCGGCCGC

39

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human apoC-II gene for
preproapolipoprotein C-II

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CGGAAGTGGG TCTCAACCAC TATAAATCCT CTCTGTGCCC GTCCGGA

47

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human apolipoprotein C-I (VLDL) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

TGCCCCGCCC CTCCCCAGCC TGATAAAGGT CCTGCGGGCA GGACAGG

47

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human apolipoprotein D gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ATCAGAGACC TGAAGAAGCT TATAAAATAG CTTGGGAGAG GCCAGTC

47

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human arginase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GGTTGTTTAT TCAACCCAAG TATAAATGGA AAAAAAAGAT GCGCC

45

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human argininosuccinate synthetase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CTGCCCCCGG GCCCTGTGCT TATAACCTGG GATGGGCACC CCTGC

45

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human sodium/potassium ATPase alpha 3 subunit (ATP1 A3)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CCCCTCCCGC GGACGCGGGC ATATGAGGAG GCGGAGGCGG CGGC

44

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human (BSF-2/IL6) gene for B cell
stimulatory factor-2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ATTAGAGTCT CAACCCCAAA TAAATATAGG ACTGGAGATG TCTGAGGC

48

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human C5 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TCTGAATTCT TCAAGTTCAG TTTATTTAAA AGGAGACTAT CCTCAAAAGT G

51

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human carbonic anhydrase II gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

CCTCCCCTTG TCGCCTAGGT CCACCCGAGC CCCCTCCCCC GGGCC

45

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human carbonic anhydrase II gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GCACGAAGTT GCGGGGAGCC TATAAAGCG GGCCGGCGCG ACCCGC

46

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human calcitonin/alpha-CGRP gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

TTCCCGACCC ACAGCGCGG GAATAAGAGC AGTCGCTGGC GCTGG

45

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human calretinin gene, exon 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CAGGCGCAGG CTCCAGAGCG TATATAAGGG CAGCGTGGCG CACAACC

47

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human cathepsin G gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

TTCCTTCCTC TCTCAGGGCC TTAAAGTCTA GGAGGAGGAA GCACA

45

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human carbonic anhydrase VII (CA VII) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CTCCTCCCGC CAGCCGCTGC TTTAAGAGGC TGCTCCGCGG TAGCG

45

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human cardiac beta myosin heavy chain gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TCTAGTGACA ACAGCCCTTT CTAAATCCGG CTAGGGACTG GGTGCC

46

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human cardiac beta myosin heavy chain gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

TGGGGGTGCC TGCTGCCCCA TATATACAGC CCCTGAGACC AGGTC

45

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human complement C3 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

TGGGGGAAAG CAGGAGCCAG ATAAAAAGCC AGCTCCAGCA GGCGCTG

47

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human recognition/surface antigen

(CD4) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CAAGTCCTCA CACAGATACG CCTGTTTGAG AAGCAGCGGG CAAGAAAGAC

50

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human hyaluronate receptor gene
(CD44)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

TAGGTCACTG TTTTCAACCT CGAATAAAAA CTGCAGCCAA CTTCCGAGGC

50

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human cystic fibrosis transmembrane
conductance reg. gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

AATGACATCA CAGCAGGTCA GAGAAAAAGG GTTGAGCGGC AGGCACCCAG

50

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human cholesterol
7-alpha-hydroxylase (CYP7) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

ATGGATCTGG ATACTATGTA TATAAAAAGC CTAGCTTGAG TCTCTT

46

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human choline acetyltransferase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

AGCAATTGTG ACCCACAGCC TAATAATAAC AGTCTTTGCC CTCTTGCC

49

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human mast cell chymase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

CTCTCTTGCC TTCTAGGAGT TATAAAACCC AAGACTGGAA AGGAAA

46

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human heart chymase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

CCTCTCTTGC CTTCTGGGAG TTATAAAACC CAAGACTGGA AGGAAAA

47

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human creatine kinase B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GGCCAATGGA ATGAATGGGC TATAAATAGC CGCCAATGGG CGGCCCGC

48

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human C-type natriuretic peptide
gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

ACATCAGCGG CAGGTTGGAT TATAAAGGCG CGAGCAGAGT CACGGG

46

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human transmembrane protein (CD59) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GCTCCGCGCG GGGGTGGAGG GAGAGGAGGA GGTTCCTGCC GAGGT

45

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human transmembrane protein (CD59) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GAGGGCAAGG GCATCCTGAG GGGCGGGGCC GGGGGCGGAG CCTTGC

46

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human transmembrane protein (CD59)
gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

ATCCTGAGGG GCGGGGCCGG GGGCGGAGCC TTGCGGGCTG GAGCGA

46

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human transmembrane protein (CD59)
gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

TGAGGGGCGG GGCCGGGGGC GGAGCCTTGC GGGCTGGAGC GAAAGAATGC

50

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human myeloid specific CD11b gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GCCCTCTTCC TTTGAATCTC TGATAGACTT CTGCCTCCTA CTTCTC

46

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human cholesteryl ester transferase
protein (CETP) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GTGGGGGCTG GCGGACATA CATATACGGG CTCCAGGCTG AACGGC

46

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human cystic fibrosis transmembrane
conductance regulator

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

TGGGTGGGGG GAATTGGAAG CAAATGACAT CACAGCAGGT CAGAG

45

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human cystic fibrosis transmembrane
conductance regulator

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GTGGGGGGGAA TTGGAAGCAA ATGACATCAC AGCAGGTCAG AGAAAAA

47

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human coseg gene for vasopressin-neurophysin precursor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CACGGGAACA CCTGCGGACA TAAATAGGCA GCCAGCAGAG GCAGCA

46

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human creatine kinase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

TTCAGAGAAA GGGCAGGTGC TATAAAGGGC CCAGCGCCAC GGGCCT

46

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human alpha-B-crystallin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

AGAAGCTTCA CAAGACTGCA TATATAAGGG GCTGGCTGTA GCTGCAG

47

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human C3 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

AGTGGGGGAA AGCAGAGCCA GATAAAAAGC CAGCTCCAGC AGGCGCTGCT

50

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human colony stimulating factor
CSF-1 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GCCTGGCCAG GGTGATTTC CATAAACCAC ATGCCCCCA GTCCTC

46

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human cytotoxic serine proteinase
gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GTTACTCAGC AGCAGGGGTG TAAATGTGAC AGTGCCATGT CAAC

44

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human CST3 gene for cystatin C

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GGCGGCGAAG GCCGGAAGGG ATAAAACCGC AGTCGCCGGC CTCGCG

46

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human CST4 gene for Cystatin D

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

TTGGGGGACA CCAAGTAGG ATAAATGCAC AGCTAGCTTC TGGCC

45

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human CYP2C8 gene for cytochrome P-450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

ACTAAATTAG CAGGGAGTGT TATAAAACT TTGGAGTGCA AGCTC

45

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human cholesterol desmolase cytochrome gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

AGCAGGAGGA AGGACGTGAA CATTTTATCA GCTTCTGGTA TGGCC

45

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human cholesterol desmolase cytochrome P-450 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

TATGGCCTTG AGCTGGTAGT TATAATCTTG GCCCTGGTGG CCCAGG

46

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human steroid 11-beta-hydroxylase (CYP11B1) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GAAGGCAAGG CACCAGGCAA GATAAAAGGA TTGCAGCTGA ACAGGGT

47

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human CYPXI gene for steroid 18-hydroxylase (P-450 C18)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

CAGAGCAGGT TCCTGGGTGA GATAAAAGGA TTTGGGCTGA ACAGGGT

47

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human CYPXIX aromatase P-450 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

TGGACAATAA ATGAAATCTC CATAAAAGGC CCAAAGGACA GGGTTC

46

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human decay-accelerating factor (DAF) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

AGCCCAGACC CCGCCCAAAG CACTCATTTA ACTGGTATTG CGGAGC

46

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human dopamine beta-hydroxylase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

ACGTCCATGT GTCATTAGTG CCAATTAGAG GAGGGCAGCA GGCTG

45

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human dopamine beta-hydroxylase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

ACCCCATTC A GGACCAGGGC ATAAATGGCC AGGTGGGACC AGAGAG

46

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human desmin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GGGGCTGATG TCAGGAGGGA TACAAATAGT GCCGACGGCT GGGGGC

46

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human cytokeratin 8 (CK8) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

CCCGGGGCTG GGATCTCTTT TATAAAAGGC CATTCCTGAG AGCTC

45

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human DNA polymerase alpha gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GCCTCCCGAG CCGCTGATTG GCTTTCAGGC TGGCGCCTGT CTCGGCCCCC

50

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human dopamine D1A receptor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

GCTGTGCCCC GCGGGAACCC CGCCGGCCTG TGCCTTGCT GGTGCCAGCT

50

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human eosinophil cationic protein
(ECP) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

AGACCCACCA AGGGAAGCTT TATTTAAACA GTTCCAAGTA GGGGAGA

47

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human HER2 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GAGGAGGAGG GCTGCTTGAG GAAGTATAAG AATGAAGTTG TGAAGCTGAG

50

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human elastin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GTGTCTCGCT GTGATAGATC AATAAATATT TTATTTTTTGG TCCTGG

46

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human endothelial leukocyte adhesion molecule I (ELAM-1)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

ATTCACAGGA AGCAATCCCT CCTATAAAAG GGCCTCAGCC GAAGTAGTG

49

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human eosinophil major basic protein gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GGAAGTTCCT CCAAGGCCTC TATATAAGAA GTCTTTGTGA GAGGAAG

47

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human preproenkephalin B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

CTCTAGGAAA GTTTCTCAGC TCTCAACCT CTGTTTCTC ATCTGCAAG

49

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human preproenkephalin B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

TTCTCATCTG CAAGATGGGG ATAATATTAA CCAACTGGCT AGGTCATGAG

50

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human ENO3 gene for muscle-specific enolase

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

GGGGACCGAG TGGCTCAGGG ATAAATGCGC ACCTGAGAGG GGGTGA

46

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human eosinophil derived neurotoxin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

CAACCCACCA AGGGATGCTT TATTTAAACA GTTCCAAGTA GGGGAGA

47

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human erythropoietin receptor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

TACCCAGGCT GAGTGCTGGC CCCGCCCCCT CGGGGATCTG CCACTT

46

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human c-erb B2/neu protein gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

AGGAGGGCTG CTTGAGGAAG TATAAGAATG AAGTTGTGAA GCTGA

45

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human ERCC2 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

CCGATTGGCT CTGCCCTAGC GGATTGACGG GCAGGTTAGC CAATGGTCT

49

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human ERCC2 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

CAGGTTAGCC AATGGTCTCG TAATATAGGT GGAGCGAGCC CTCGAGG

47

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human erythropoietin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

GGTCACCCGG CGCGCCCCAG GTCGCTGAGG GACCCCGGCC AGGCGCGGAG

50

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human oestrogen receptor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

ATATGAGCTC GGGAGACCAG TACTTAAAGT TGGAGGCCCG GGAGCCCA

48

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human elastase I gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

AGCTTTGCTG CTAAGAGGAG TATAAAGAGG GCTTGGTCCA AGCAAG

46

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human fibrinogen gamma chain gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GGCCCCGTGA TCAGCTCCAG CCATTTCAG TCCTGGCTAT CCCA

44

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human fibrinogen gamma chain gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

TGGCTATCCC AGGAGCTTAC ATAAAGGGAC AATTGGAGCC TGAGA

45

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human lymphocyte IgE receptor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

TTAACATCTC TAGTCTCAC CCAATTCTCT TACCTGAGAA ATGGA

45

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human lymphocyte IgE receptor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

GTTATCCGGG TGGCAAGCCC ATATTAGGT CTATGAAAAT AGAAGCT

47

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human lymphocyte IgE receptor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

AGCCCATATT TAGGTCTATG AAAATAGAAG CTGTCAGTGG CTCTAC

46

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human apoferritin H gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GGGCCTGACG CCGACGCGGC TATAAGAGAC CACAAGCGAC CCGCA

45

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human fibrinogen beta gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

TATTAATAA GGAAAGGTAA CCATTTCTGA AGTCATTCCT AGCAGA

46

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human fibrinogen beta gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

ATTCCTAGCA GAGGACTCAG ATATATATAG GATTGAAGAT CTCTCAGTT

49

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human factor IX gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

CCAGAAGTAA ATACAGCTCA GCTTGTACTT TGGTACAACCT AATCGACCTT

50

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human FK506 binding proteins 12A,
12B, and 12C (FKBP12)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

GAGCCGTGGA ACCGCCGCCA GGTCGCTGTT GGTCCACGCC GCCCGTCGCG

50

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human 5-lipoxygenase activating protein (FLAP) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

TTGTGCCGGG GATCTTCAGA AATTGTAATG ATGAAAGAGT GCAAGCTCTC

50

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human fos proto-oncogene (c-fos)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

ATTCATAAAA CGCTTGTTAT AAAAGCAGTG GCTGCGGCGC CTCGTACTCC

50

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human GOS2 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GGCGTGTCTC AGAGAAAAGA TATAAGCGGC CCCC GGACGC TAAAG

45

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human granulocyte colony-stimulating
factor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

CAGGCCTCCA TGGGGTTATG TATAAAGGGC CCCCTAGAGC TGGGCC

46

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human EGR2 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

CGGGTATTGA AGACCTGCCC ATAAATACTT AGAGCAACAC TTTCCGTC

48

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human growth hormone (hGH) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

TGGGAGAGAA GGGGCCAGGG TATAAAAAGG GCCCACAAGA GACCAG

46

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human gastric inhibitory polypeptide (GIP) mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

TAATCAGCAG GTCTATGCCT AATATAAAGG AGCTGGGGCA TGATTCTTC

50

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human GLA gene for alpha-D-galactosidase A

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GAAACAATAA CGTCATTATT TAATAAGTCA TCGGTGATTG GTCCGC

46

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human glucagon gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

TTTACAGATG AGAAATTTAT ATTGTCAGCG TAATATCTGT GAGG

44

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human glucagon gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

GGCTAAACAG AGCTGGAGAG TATATAAAAG CAGTGCGCCT TGGTGCA

47

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human granulocyte-macrophage colony stimulating factor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

CATTAATCAT TTCCTCTGTG TATTTAAGAG CTCTTTTGCC AGTGAGC

47

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human glucocorticoid receptor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

TGGGCAATGG GAGACTTTCT TAAATAGGGC TCTCCCCCA CCCATG

46

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human growth hormone releasing factor (GRF) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

AACGCTTAGG AAAATGAAGA GATAAATGAT GGGAACGCCA GCGGCTGCC

50

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human GST pi gene for glutathione S-transferase pi

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GAGCGGGGCG GGACCACCCT TATAAGGCTC GGAGGCCGCG AGGC

44

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: human glycoporphin C (GPC) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

CAGAAGTGGG CGGGTGTGTG TTTAAAAAAA AAAAAAGGGG TGGAAC

47

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human histone (H10) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

CGCGGTCCGC CCGCCGCCGC TAAATACCCG GATGCGCCGC CCAAGC

46

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene for H1 RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GTCTTTGGAT TTGGGAATCT TATAAGTTCT GTATGAGACC ACTC

44

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human H1 histone gene FNC16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GGCGGTGGAT TGGACGCTCC ACCAATCACA GGCAGCGCC GGCTTA

46

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human histone gene FNC16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

ACCAATCACA GGCAGCGCC GGCTTATATA AGCCCGGGCC CGAGCATAGC AGCA

54

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human H2B.2 and H2A.1 genes for
Histone H2A and H2B

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

TTTTCGCGCC CAGCAGCTGC TATAAAATGC GCGTCCCTGT AGGTTCC

47

(2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human H4/a gene for H4 histone

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

GGGGGCAGGG GTAACGTAGA TATATAAAGA TCGGTTTCCT ATTCTCTC

48

(2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human H4/b gene for H4 histone

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

CTGCAAGTAT AGTGTGTGTG TATATATATA TATATACCTA GCAGTATTTA TTAAAT

56

(2) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human androgen receptor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

GGTGGGGGCG GGACCCGACT CGCAAACGTG TGCATTGCT CTCCACCTCC

50

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human chorionic gonadotropin (hCG)
beta subunit

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

GCCCTCTCTC ATTGGGCAGA AGCTAAGTCC GAAGCCGCGC CCCTCCTGG

49

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human islet amyloid polypeptide
(hIAPP) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

GCTGAGAAAG GTGTGAGGGG TATATAAGAG CTGGATTACT AGTTAGCAAA

50

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human H4 histone gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

CTTCCCGCCG GCGCGCTTTC GGTTTTCAAT CTGGTCCGAT ATCTCTGTAT AT

52

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human H4 histone gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

AATCTGGTCC GATATCTCTG TATATTACGG GGAAGACGGT GACGCTC

47

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human histone H2a gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

TCCTCTTTTC TTGGCGAACT CAACTGGTAT GAATTCCTCA

40

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human histone H2a gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

CACAGCCTAC CTCCAGTCAG TATAAATACT TCTCTGCCTT GCGTTC

46

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human histone H2b gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

TATTTGCATA AGCGATTCTA TATAAAAGCG CCTTGCATA CCCTGCT

47

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human histone H3 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

ATTTTGAAT TTTCTTGGGT CCAATAGTTG GTGGTCTGAC TCTAT

45

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human histone H3 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

CAATAGTTGG TGGTCTGACT CTATAAAAGA AGAGTAGCTC TTTCCTT

47

(2) INFORMATION FOR SEQ ID NO:171:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human HLA-A1 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

AGTGTCGTCG CGGTCGCTGT TCTAAAGTCC GCACGCACCC ACCGG

45

(2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human HLA-B27 antigen gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

AGTGTCGCCG GGGTCCCAGT TCTAAAGTCC CCACGCACCC ACCCGG

46

(2) INFORMATION FOR SEQ ID NO:173:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human HLA-Bw57 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

AGCGTCGCCG CGGTCCCAGT TCTAAAGTCC CCACGCACCC ACCCG

45

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human HLA-F gene for human leukocyte antigen F

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

TGTCGCCGCA GTTCCCAGGT TCTAAAGTCC CACGCACCCC GCGGGA

46

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human gene for histocompatibility antigen HLA-A3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

AGTGTCTGTCG CGGTGCTGT TCTAAAGCCC GCACGCACCC ACCGGG

46

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human gene for class I histocompatibility antigen HLA-CW3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

CATTGGGTGT CGGACCTCTA GAAGGCCGGT CAGCGTCTCC GC

42

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human HMG-17 gene for non-histone chromosomal protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

CGGTCCGGGG CTCCCAGCGC TATAAAACT TTATAAACCC CCCGGA

46

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human HOX3D gene for homeoprotein HOX3D

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

AAGAAAGAGA TATCTCCACC TATAAATTGT CCACTTTGGA GAACAA

46

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human 71Kd heat shock cognate protein (hsc70)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

TGGAAGGTC TAAGATAGGG TATAAGAGGC AGGGTGGCGG GCGGA

45

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human heat shock protein (hsp 70) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

AAGGCGGGTC TCCGTGACGA CTTATAAAAG CCCAGGGGCA AGCGGTCCGG

50

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human hsp70B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

CTTCGGTCTC ACGGACCGAT CCGCCCGAAC CTTCTCCCGG GGTCAG

46

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human hsp70B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

CCGCCCCGGCT GACTCAGCCC GGGCGGGCGG GCGGGAGGCT CTCGAC

46

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human hsp70B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

CCGGCTGACT CAGCCCGGGC GGGCGGGCGG GAGGCTCTCG ACTGGG

46

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human hsp70B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

CTGACTCAGC CCGGGCGGGC GGGCGGGAGG CTCTCGACTG GGCGGG

46

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human hsp70B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

GGGCGGGCGG GAGGCTCTCG ACTGGGCGGG AAGGTGCGGG AAGGT

45

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human hsp70B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

CGGCGGGGTC GGGGAGGTGC AAAAGGATGA AAAGCCCGTG GACGGAGCTG AGC

53

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human IAPP gene for islet amyloid polypeptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

GCTGAGAAAG GTGTGAGGGG TATATAAGAG CTGGATTACT AGTTAGC

47

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human intercellular adhesion molecule 1 (ICAM-1) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

AGGTTTCCGG GAAAGCAGCA CCGCCCCTTG GCCCCCAGGT GGCTAG

46

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human intercellular adhesion molecule 1 (ICAM-1) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

46

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

48

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

48

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human interferon alpha gene
IFN-alpha 16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

GAAATTAGTA TGTTCACTAT TTAAGAACTA TGCACAGAGC AAAGT

45

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human interferon alpha gene
IFN-alpha 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

ATGGAAACTC GTATGTGACC TTTTAAAGAT CTGTGCACAA AACAAGGT

48

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human interferon alpha gene
IFN-alpha 6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

ATGGAAACTA GTATGTTCCC TATTTAAGAC CTACACATAA AGCAAGGT

48

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human interferon alpha gene
IFN-alpha 7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

ATGGAAATTA GTATGTTTAC TATTTAAGAC CTATGCACAG AGCAAAGT

48

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human immune interferon (INF-gamma)
gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

TCCTCAGGAG ACTTCAATTA GGTATAAATA CCAGCAGCCA GAGGAGGTGC

50

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human alpha/beta-interferon
(IFN)-inducible 6-16 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

GGGAGGATCC ACAAGTGATG ATAAAAAGCC AGCCTTCAGC CGGAG

45

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human insulin like growth factor II (IGF-2)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

CTGGGAGGAG TCGGCTCACA CATAAAAGCT GAGGCACTGA CCAGCCT

47

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human insulin-like growth factor binding protein gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

GTGGCGCGGC CTGTGCCCTT TATAAGGTGC GCGCTGTGTC CAGCG

45

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human germline leader peptide and variable region of 1154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

CAACCTCCTG CACTGAAGCC TTATTAATAG GCTGGCCACA CTTCATGC

48

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human germline for leader peptide & variable region of 2908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201: .

CAACCTCCTG CCCTGAAGAC TTATTAATAG GCTGGACACA CTTCATGC

48

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human rearranged kappa immunoglobulin subgroup V

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

CCACGACCAG GTGTTTGGAT TTTATAAACG GGCCGTTTGC ATTGTGAA

48

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human rearranged kappa
immunoglobulin gene subgroup V

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

CGCCCTGCAG TCCAGAGCCC ATATCAATGC CTGGGTCAGA GCTCTGGA

48

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human germline fragment for
immunoglobulin kappa light chain

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

TGCCCTACCT TCCAGAGCCC ATATCAATGC CTGTGTCAGA GCCCTGGG

48

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human germline immunoglobulin kappa
light chain V-segment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

ACTTCCCTTG TGGGTCTGAG ATAAAAGCTC AGCTCTAACC CTTACC

46

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human interleukin-2 (IL-2) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

TATTTTCCA GAATTAACAG TATAAATTGC ATCTCTTGTT CAAGAG

46

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene for interleukin 1 alpha
(IL-1 alpha)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

CCACGCCTAC TTAAGACAAT TACAAAAGGC GAAGAAGACT GACTCAG

47

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene for prointerleukin 1 beta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

TTGATTGTGA AATCAGGTAT TCAACAGAGA AATTTCTCAG CCTCCTAC

48

(2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human gene for prointerleukin 1 beta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

CTACTTCTGC TTTTGAAAGC TATAAAAACA GCGAGGGAGA AACTGGC

47

(2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: human interleukin 2 receptor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

AGAAAGGATT CATAAATGAA GTTCAATCCT TCTCATCACC CCAGCCCA

48

(2) INFORMATION FOR SEQ ID NO:211:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human interleukin 2 receptor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

TTTGAAAAAT TACCGCAAAC TATATTGTCA TCAAAAAAAAA AAAAAA

46

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human interleukin 4 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

ATCTGGTGTA ACGAAAATTT CCAATGTAAA CTCATTTTCC CTCGG

45

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human interleukin 4 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

GGTTTCAGCA ATTTTAAATC TATATATAGA GATATCTTTG TCAGCATT

48

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human interleukin 5 (IL-5) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

CATTCCTCA AAGACAGACA ATAAATTGAC TGGGGACGCA GTCTGTACT

50

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human interleukin 7 (IL-7) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215: .

TTGCTTTGAT TCAGGCCAGC TGGTTTTTCT GCGGTGATTC GGAAATTCGC

50

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human interleukin 9 gene (IL-9)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

TTCCGTGTTT GAGAGGGAGC TTAAATACC ACTCGATTG AAGGTGTC

48

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human int-1 mammary oncogene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

ACTTCAGCCA GCGCCGCAAC TATAAGAGGC GGTGCCGCC CCGT

45

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human jun-B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

TCCGTGGCTG ACTAGCGCGG TATAAAGGCG TGTGGCTCAG GCTGAG

46

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human DNA for 65 kD keratin type II

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

GCCCAACAAC CTCCTCAAAT GTATATAAAG GGATTTTAT TGCACA

46

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human ultra high-sulphur keratin
protein gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

TGGTGTGTTC CTATGTGGGA TATAAAGAGC CGGGGCTCAG GGGGCT

46

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human alpha-lactalbumin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

CCTGAGGCTT TCTGCATGAA TATAAATAAA TGAACTGAG TGATGCT

47

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human LAG-1 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

GTCCTAGGCC TCAGAGTCCC TATAAGAGAG ATTCCCAACT CAGTA

45

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human lecithin-cholesterol
acyltransferase (LCAT) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

CTGAGGCTGT GCCCCTTTCC GGCAATCTCT GGCCACAACC CCCACTGG

48

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human lecithin-cholesterol
acyltransferase (LCAT) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

CCCCTCCCAC TCCCACACCA GATAAGGACA GCCCAGTGCC GCTTT

45

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human lymphocyte-specific protein
kinase (lck) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

GGGAGCAGAT CTTGGGGGAG CCCCTTCAGC CCCCTCTTCC ATTCCCTCAG

50

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human leukocyte fuction-associated antigen-1 (LFA-1) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

GGGTATCTCA CTGTGGTTTG ATTTGCATTT CTCTAATGAC TAATAGTG

48

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human leukocyte fuction-associated antigen-1 (LFA-1) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

ATGTCTCTAA CTTGCTTACA CTTCTCCCT GAACCCTGCG GTTTCA

46

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human leukocyte function-associated
antigen-1 (LFA-1) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

TCCTGCAGGC ACACCTCCCT CCCCGCCTGC CAGTGCACC AGCCTGTT

48

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human leukocyte function-associated
antigen-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

CTGTTGCCTC TGTGAGAAAG TACCACTGTA AGAGGCCAAA GGGCATGATC

50

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: human lipoprotein lipase (LPL) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

TATTTGCATA TTTCCAGTCA CATAAGCAGC CTTGGCGTGA AAACAGT

47

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human leukocyte adhesion molecule-1
(LAM-1)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

TGGGTTAGAG AAATGAAAGA AAGCAAGGCT TTCTGTTGAC ATTCAGTGCA

50

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human lysozyme gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

AGAAGGAAGT TAAAAGATGT TAAATACTGG GGCCAGCTCA CCCTGG

46

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human mannose binding protein 1
(MBP1) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

AGGGATGGGT CATCTATTTT TATATAGCCT GCACCCAGAT TGTAGG

46

(2) INFORMATION FOR SEQ ID NO:234:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human mast cell carboxypeptidase A (MC-CPA) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

CATCAAGATA AGGGCTGAGG CATAAACTG CCAGAGGGTC TCAAGG

46

(2) INFORMATION FOR SEQ ID NO:235:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human P-glycoprotein (MDR1) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

CTTGCCACA GGAAGCCTGA GCTCATTCGA GTAGCGGCTC TTCCA

45

(2) INFORMATION FOR SEQ ID NO:236:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human bone marrow serine protease gene (medullasin)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

ACGGCCTCCC AGCACAGGGC TATAAGAGGA GCCGGGCGGG CACGG

45

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human microsomal epoxide hydrolase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

TTGCTGTGCA GAGTCCAGGG GAGATAACCA CGCTGTGCAC ACATGAG

47

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human metallothionein-Ie gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

GCAGCCAGTT GCAGGGCTCC ATTCTGCTTT CCAACTGCCT GACTGCTTGT TC

52

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human myoglobin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

TTGTCAAGCA TCCCAGAAGG TATAAAAACG CCCTTGGGAC CAGGCA

46

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human melanoma growth stimulatory
activity (MGSA) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

GCTTCCAGC CCCAACCATG CATAAAAGGG GTTCGCGGAT CTCGGAG

47

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human alpha-MHC gene for myosin
heavy chain (N-terminus)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

AGAGGGTGGG GGAAACGGGA TATAAAGGAA CTGGAGCTTT GAGGAG

46

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human class II invariant gamma-chain gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

GATTCCTCTC CAGCACCGAC TTAAAGAGGC GAGCCGGGGG GTCAG

45

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human motilin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

CCCAGGGTTG GGAGGTATAT AAGAACCCGT CAGATCAGCC G

41

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human myeloperoxidase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

CCACCCCCAG CTTAGAGGAC ATAAAAGCGC AGATTGAGCT AAGAGGAGCT

50

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs

46

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human neuromedin K receptor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

GAAGCGTGGG ACCCCATGAG TATAAAGAGA GCCTGTAGCG CAGG

44

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human gene for heavy neurofilament subunit (NF-H) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

TTGGACCCGG CCGCGGCGGC TATAAAAGGG CCGGCGCCCT GGTCGT

46

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human nuclear factor NF-IL6 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

CGGTTGCTAC GGGCCGCCCT TATAAATAAC CGGGCTCAGG AGAAACT

47

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human neurofilament subunit NF-L gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

TGCGTCAGGA CCTCCCGGCG TATAAATAGG GGTGGCAGAA CGGCGC

46

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human neurokinin-2 receptor (NK-2) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

TCTCTTCAGC GAAGGGGTTG ATTTATAAGG GTGTTTTCTG CTCTGACA

48

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human n-myc gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

GGGTGTGTCA GATTTTTCAG TTAATAATAT CCCCCGAGCT TCAAAGCGC

49

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human ornithine decarboxylase (ODC1)
gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

CCATGGCGAC CCGCCGGTGC TATAAGTAGG GAGCGGCGTG CCGTGG

46

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human ornithine transcarbamylase
(OTC) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

ATACACAGCG GTGGAGCTTG GCATAAAGTT CAAATGCTCC TACACC

46

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human prepro-oxytocin-neurophysin I gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

CTCCACCGAC GCAATGCCCA GGCATAAAAA GGCCAGGCCG AGAGACCGCC

50

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human cytochrome P450scc gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

TATGGCCTTG AGCTGGTAGT TATAATCTTG GCCCTGGTGG CCCAG

45

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human p53 gene for transmembrane related p53

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

CCCCTCCCAT GTGCTCAAGA CTGGCGCTAA AAGTTTTGAG CTTCTCAAAA

50

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human Alzheimer's disease amyloid A4 precursor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

GGGAGGCCTG CGGGGTCGGA TGATTCAAGC TCACGGGGAC GAGCAGG

47

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human Alzheimer's disease amyloid A4 precursor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

CGGGGACGAG CAGGAGCGCT CTCGACTTTT CTAGAGCCTC AGCGTCCTAG GACT

54

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human Alzheimer's disease amyloid A4 precursor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

GCGGGGTGGG CCGGATCAGC TGA CTCGCCT GGCTCTGAGC CCCGCCGC

48

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human Alzheimer's disease amyloid A4 precursor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

CCGCCGCCGC GCTCGGGCTC CGTCAGTTTC CTCGGCAGCG GTAGGCGAG

49

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human gene for plasminogen activator inhibitor 1 (PAI-1)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

TATTTCTGTC CCACATCTGG TATAAAAGGA GGCAGTGGCC CACAGAG

47

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human platelet-derived growth factor
A-chain (PDGF) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

AGGGGCGCGG CGGCGGCGGC TATAACCCTC TCCCCGCCGC CGGCC

45

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human PGP9.5 gene for
neuron-specific ubiquitin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

ACAGTGCCTC TGGCCGGCGC TTTATAGCTG CAGCCTGGCG CTCCGC

46

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human plasminogen gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

CTCCACCGAC GCAATGCCCA GGCATAAAAA GGCCAGGCCG AGAGACCGCC

50

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human phenylethanolamine N-methylase (PNMT) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

TCGGGGCGGG GGTCTGGGCGG TAGAAAAAAG GGCCGCGAGG CGAGCGGGG

49

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human opiomelanocortin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

CTCCCCGTGT GCAGACGGTG ATATTTACCG CCAAATGCGA ACCAGGC

47

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human gene PRB3L for proline-rich protein G1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

GCCACTGTTC TGCTCCTCTT TATAAAGGGA GCTGCCATGG TTCTCC

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(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human PRB4 gene for proline-rich protein Po

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

CATTGTTTTG CTCCTCTTTA TAAAGGGAGT TGCCACGTTC CTCC

44

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human prolactin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

AGGCTTTGAT ATCAAAGGTT TATAAAGCCA ATATCTGGGA AAGAGA

46

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human prothymosin-alpha gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

CCGAGCGCCG CCCACTAATC TATATTAAAG CTTCTGGCGC CGCGTG

46

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human protamine 2 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

TCATAGTGGG CGTCCCCCTT TATATACAAG CTCCCGGGGA GCCTTG

46

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human SPR2-1 gene for small proline rich protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

CTGGGTGGGG TAGCAGGCTC TATAAAGAGA TCCTCTGCTG CACGAC

46

(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human estrogen-responsive gene pS2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

TAAGCAAACA GAGCCTGCCC TATAAAATCC GGGGCTCGGG CGGCCTC

47

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human pulmonary surfactant
apoprotein (PSAP) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

AGCCTGGCAG CCCCCACATC TATAAATGCT GCGTCTACCT TACCCT

46

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene for prostatic secretory
protein PSP-94

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

TGCGTGTTG CCCTCTCCAG TATAAAAGTT TGATGCAGCT TTTCC

45

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human parathyroid hormone-related peptide (PTHRP) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

GAGGTAGACA GACAGCTATG TATATATATG TGGGTTTCGC TACAAGTGG

49

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene for purine nucleoside phosphorylase

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

CTGGGGACTC CAGGGCAAGG GATATAAGCC AGAGCCTAGA CCAGTG

46

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human rDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

ATTTTGGGCC GCCGGGTAT

20

(2) INFORMATION FOR SEQ ID NO:281:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human regenerating protein (reg) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

GTTCTTATCT CAGATCCTGA TATAAAGCTC CTACAGCTAC CTGGCC

46

(2) INFORMATION FOR SEQ ID NO:282:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human renin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

ATCACCCCAT GCATGGAGTG TATAAAAGGG GAAGGGCTAA GGGAGCC

47

(2) INFORMATION FOR SEQ ID NO:283:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human gene fragment for retinol binding protein (RBP)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

CGACCCCCTC CCCCCGGCGC TATAAAGCAG CGGGGCGGCC GCGGCG

46

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human serum amyloid A (GSAA1) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

CACCCCGCTA ATTTAAAAAA TATATATACA GATATATAGT GGAGATGG

48

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human SAA1 beta gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

AACCAGCAGG GAAGGCTCAG TATAAATAGC AGCCACCGCT CCCTGGC

47

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene fragment for HLA class II
SB 4-beta chain

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

CTACTTGGGT TCATGGTCTC TAATATTTCA AACAGGAGCT CCCTTTAG

48

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human c-sis proto-oncogene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

TCGCACTCTC CCTTCTCCTT TATAAAGGCC GGAACAGCTG AAAGGG

46

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human SLPI gene for secretory
leukocyte protease inhibitor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

CACACCCACT GGTGAAAGAA TAAATAGTGA GGTTCGCAT TGGCCA

46

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human superoxide dismutase (SOD-1)
gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

CGAGGCGCGG AGGTCTGGCC TATAAAGTAG TCGCGGAGAC GGGGTG

46

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human ornithine decarboxylase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

TCCATGGCGA CCCGCCGGTG CTATAAGTAG GGAGCGGCGT GCCGT

45

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human steroid 5-alpha-reductase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

CTGCCCCCGC GCCGCCGCC TATATGTTGC CCGCCGCGGC CTCTG

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(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human substance P receptor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

GTGACGTCTC TGCAGGGGGT TATAAAAGCC TCGTGCGCAG CTAA

44

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human synaptobrevin 1 (SYB1) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

CCGGGAGGCG TGGTCAGCAC TAATAAAGGC GGAGGCCGGC GCGGCA

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(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human tyrosine aminotransferase
(TAT) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

CAACGCCCAT TTGTGGAGAC TATTCAGGA GTTAGGATTT GCATCTG

47

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human T-cell receptor V-beta gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

GACAGATGCA TTCTGTGGGG ATAAATGTC ACAAATTC TTTCTTT

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(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human T-cell receptor V-beta gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

TCACAGAGGG CCTGGTCTAG AATATCCAC ATCTGCTCTC ACTCT

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(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human T-cell receptor V-beta gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

GACAGATGCA TTCTGTGGGG ATAAAATGTC ACAAATTCA TTTCTTT

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(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human T-cell receptor V-beta gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

TCACAGAGGG CCTGGTCTGG AATATTCCAC ATCTGCTCTC ACTCTG

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(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human T-cell receptor V-beta chain gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

TGTTACTGTA GGAAC TACCG TATAAGGACA GGATGTCCCA CCTCC

45

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human transferrin (Tf) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

CCGCCCAGGC CGGGAATGGA ATAAAGGGAC GCGGGGCGCC GGAGG

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(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human interleukin 3 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

GGGCACCTTG

10

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human tissue factor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

CGGGAGAGCG CGCCGCCGGC CCTTTATAGC GCGCGGGGCA CCGGCTCCCC

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(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human transforming growth factor-beta (TGF-beta)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

TGCCTTGCCC ATGGGGGCTG TATTTAAGGA CACCGTGCCC CAAGCCC

47

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human transforming growth factor beta-3 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

GAGACGTCAT GGGAGGGAGG TATAAAATTT CAGCAGAGAG AAATAGA

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(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human transforming growth factor beta-2 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

CACGTGGTTC AGAGAGAACT TATAAATCTC CCCTCCCCGC GAAGA

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(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human tyrosine hydroxylase (TH) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

GGCTTTGACG TCAGCTCAGC TTATAAGAGG CTGCTGGGCC AGGGCT

46

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human metallothionein gene IIA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

TCGTCCCGGC TCTTTCTAGC TATAAACACT GCTTGCCGCG CTGCAC

46

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human thrombospondin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

CCCAGGAATG CGAGCGCCCC TTAAAAGCG CGCGGCTCCT CCGCCT

46

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human thyroxine-binding globulin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

ATAATGTTGC TATAACATCT GAATGACAGT CCATGGCATT ATTTC

45

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human thyroglobulin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

GAAAGTGCCA ACGGCAGCTC TATAAAAGCT CCCTGGCCAG GGGACCT

47

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human gene for tumor necrosis factor (TNF-alpha)

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(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human triosephosphate isomerase
(TPI) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

AGTTCCAATT CGCGGCGCTC TATATAAGTG GGCAGTGGCC GGAAGTGC

47

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human thyroid peroxidase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

ATCCAAGCGC AGAGTCAGTT TATAAGGTGG GTAACCAAGT CCCT

44

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human transferrin receptor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

GGCCGGGGGC GGGGCCAGGC TATAAACCGC CGGTTAGGGG CCGCCA

46

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human tryptase -I gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

CGCCCCCTCC TGATCTGGAA GGATAAATGG GGAGGGGAGA GCCACTGGGT

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(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human beta 2 gene for beta-tubulin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

GCGGAGGCGG GCAGGGAGGG TATATAAGCG TTGGCGGACG GTCGGT

46

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene for U 6 RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

GTATTCGAT TTCTTGGCTT TATATATCTT GTGGAAAGGA CGAAAC

46

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human uPA gene for
urokinase-plasminogen activator

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

GGCGGCGCCG GGGCGGGCCC TGATATAGAG CAGGCGCCGC GGGTCGC

47

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human proto-oncogene vav

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

GCAGGCGTGC GGGCGGGTGG GTGGTGGAGG CTGCGA

36

(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human vascular cell adhesion
molecule-1 (VCAM1) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

GCCTCTGCAA CAAGACCCTT TATAAAGCAC AGACTTTCTA TTTC

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(2) INFORMATION FOR SEQ ID NO:323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human vimentin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

ACCCTCTTTC CTAACGGGGT TATAAAAACA GCGCCCTCGG CGGGG

45

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human U1 RNA gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

GTAAAGGGTG AGGTATATGG AGCTGTGACA GGCAGAAAGT GTGTGAAGTC

50

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene for small nuclear U1 RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

GTAAAGAGTG AGGCGTATGA GGCTGTGTCG GGGCAGAGGC CCAAGATCTC

50

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human small nuclear U2 RNA gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

TTGAATGTGG ATGAGAGTGG GACGGTGACG GCGGGCGCGA AGGCGAGCGC

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(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human U3 small nuclear RNA gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

AAAAGTTTGC GGCAGATGTA GACCTAGCAG AGGTGTGCGA GGAGGCCGTT

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(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human U4C small nuclear RNA gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

AAATGGTAGT CATCATCCGT GGGGGAGCGG GCGCGAATA AAGCCTTTCC

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(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human histone H3.3 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

GGGCGGGGCG GCGTGTGTTG GGGGATAGCC TCGGTGTCAG CCATCTTTCA

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(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human histone H4 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

AGTTCGGTCC GCCAACTGTC GTATAAAGGC GTCGCCTCAG GTCAGAGGCC

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(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human non-histone chromosomal
protein HMG-14 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

TGGGGGGCGG CCCGGCCGGC GGGGAGGGGG AGCCGCGGCC GGGACGCGGG

50

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human ribosomal protein S14 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

AAGTAATAAA CCGTCTTTC TTATGACGAG TCTTAACTC TTTGGGAGGA

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(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene for alpha tubulin (b
alpha 1)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

CGCGACCGAG GGTCTGGGCG TCCCGGCTGG GCCCGTGTC TGTGCGCACG

50

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human skeletal alpha-actin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

AGGGAATCGC CCGCGGGCTA TATAAACCT GAGCAGAGGG ACAAGCGGCC

50

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human epidermal 67-kDa Keratin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

GGAAGATCTT GTGTGATAAA ACAATTACCA CATGAACCAA TCTTGCATGC

50

(2) INFORMATION FOR SEQ ID NO:336:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human 50 KDatype I epidermal keratin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

GACCCGCCCC CTACCCATGA GTATAAGCA CTCGCATCCC TTTGCAATTT

50

(2) INFORMATION FOR SEQ ID NO:337:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human alpha-1 collagen type I gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

CTGCTCTCCA TCAGGACAGT ATAAAAGGGG CCCGGGCCAG TCGTCGGAGC

50

(2) INFORMATION FOR SEQ ID NO:338:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human collagen type-III gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

GTGAGGGAAG CCAAACCTTTT TCCTATTTAA GGCCAAAGCA AAGGAATCTC

50

(2) INFORMATION FOR SEQ ID NO:339:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human pro-alpha-2 (I) mRNA for
collagen N-prepropeptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

CAGGGAAACT TTTGCCGTAT AAATAGGGCA GATCCGGGAT TTGTTATTTT

50

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human fibronectin (FN) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

TCCAGAGGGG CGGGAGGGCC GTCCCATATA AGCCCGGCTC CCGCGCTCCG

50

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human von Willebrand factor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

TGTTTCCTTT TGGTAATTAA AAGGAGGCCA ATCCCCTGTT GTGGCAGCTC

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(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human gene for fibrinogen gamma chain

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

TGGCTATCCC AGGAGCTTAC ATAAAGGGAC AATTGGAGCC TGAGA

45

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human gene for fibrinogen gamma chain

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

CAGTCCTGGC TATCCAGGA GCTTACATAA AGGGACAATT GGAGCCTGAG

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(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human involucrin mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

AGGCCAGGCT GCAGAAATGAT ATAAAGAGTG CCCTGACTCC TGCTCAGCTC

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(2) INFORMATION FOR SEQ ID NO:345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human apolipoprotein A-I and C-III
genes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

CCAGACCCTG GCTGCAGACA TAAATAGGCC CTGCAAGAGC TGGCTGCTTA

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(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human apolipoprotein B-100 (apoB)
gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

GCTCTTGCA G CCTGGGCTTC CTATAAATGG GGTGCGGGCG CCGGCCGCGC

50

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human apolipoprotein A-I and C-III
genes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

TCTAGGGATG AACTGAGCAG

20

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Humanapolipoprotein A-I and C-III genes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

ACAGGCAGGA GGGTTCTGAC CTGTTTTATA TCATCTCCAG GGCAGCAGGC A

51

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human albumin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

TACAATTATT GGTAAAGAA GTATATTAGT GCTAATTTC CTCCGTTTGT

50

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human albumin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

TACAATTATT GGTAAAGAA GTATATTAGT GCTAATTTC CTCCGTTTGT C

51

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human serum prealbumin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

CCTAGCTCAG GAGAAGTGAG TATAAAAGCC CCAGGCTGGG AGCAGCCATC

50

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human alpha-fetoprotein (AFP) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

TAACAGGCAT TGCCTGAAAA GAGTATAAAA GAATTCAGC ATGATTTTCC

50

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human C-reactive protein gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

AGGCAGGAGG AGGTAGCTCT AAGGCAAGAG ATCTGGGACT T

41

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human gene A for alpha 1-acid glycoprotein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

AAGTGACCGC CCATAGTTTA TTATAAAGGT GACTGCACCC TGCAGCCACC

50

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human gene A for alpha 1-acid glycoprotein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

AAGTGACCGC CCATAGTTTA TTATAAAGGT GACTGCACCC TGCAGCCACC A

51

(2) INFORMATION FOR SEQ ID NO:356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene for L apoferritin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

CGGCGCACCA TAAAAGAAGC CGCCCTAGCC ACGTCCCCTC

40

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene for L apoferritin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

CGGCGCACCA TAAAAGAAGC CGCCCTAGCC ACGTCCCCTC G

41

(2) INFORMATION FOR SEQ ID NO:358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Olive baboon alpha-1 globin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

GGCGTGCCCC CGCGCCCGGA GCATAAACCC TGGCGCGCTC GCGGCCCGGC

50

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Olive baboon alpha-1 globin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

GGCGTGCCCC CGCGCCCGGA GCATAAACCC TGGCGCGCTC GCGGCCCGGC A

51

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human alpha-globin germ line gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

GTGCCAACAA TGGAGGTGTT TACCTGTCTC AGACCAAGGA CCTCTCTGCA

50

(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Chimpanzee gene for alpha-like
zeta-1-globin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

CCTGGCTGGG CCCAGCTCCC TGTATATAAG GGGACCCTGG GGGCTGAGCA

50

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

50

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Macaque cynomolgus beta-globin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

GCAGGAGCCA GGGCTGGGCA TAAAAGTCAG GGCAGAGCCA TCTATTGCTT

50

(2) INFORMATION FOR SEQ ID NO:366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Chimpanzee beta-globin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

GCAGAAGCCA GGGCTGGGCA TAAAAGTCAG GGCAGAGCCA TCTATTGCTT

50

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human germ line gene for beta-globin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

GCAGGAGCCA GGGCTGGGCA TAAAAGTCAG GGCAGAGCCA TCTATTGCTT

50

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Spider monkey (A.geoffroyi)
delta-globin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

CAGGGAGAAC AGGACCAGCA TAAAAGGCAG GGCAGGGCTA ACTGTTGCTT

50

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human transferrin receptor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

GGGCGGGGCC AGGCTATAAA CCGCCGGTTA GGGGCCGCCA TCCCCTCAGA

50

(2) INFORMATION FOR SEQ ID NO:370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human beta-2-adrenergic receptor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

AGTTCCCCTA AAGTCCTGTG CACATAACGG GCAGAACGCA CTGCGAAGCG

50

(2) INFORMATION FOR SEQ ID NO:371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human IgE receptor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

GGTGGCAAGC CCATATTTAG GTCTATGAAA ATAGAAGCTG TCAGTGGCTC

50

(2) INFORMATION FOR SEQ ID NO:372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human oncogene c-fos

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

TTCATAAAAC GCTTGTTATA AAAGCAGTGG CTGCGGCGCC TCGTACTCCA

50

(2) INFORMATION FOR SEQ ID NO:373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human c-myc oncogene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

AATCTCCGCC CACCGGCCCT TTATAATGCG AGGGTCTGGA CGGCTGAGGA

50

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human B-cell leukemia/lymphoma 2
(bcl-2) proto-oncogene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

CCGCCCCCTCC GCGCCGCCTG CCCGCCCGCC CGCCGCGCTC CCGCCCCCGG

50

(2) INFORMATION FOR SEQ ID NO:375:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human p53 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

ACTCCATTTC CTTTGCTTCC TCCGGCAGGC GGATTACTTG CCCTTACTTG

50

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human gene homologous to bladder carcinoma oncogene T24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

CGCGGCCCTA CTGGCTCCGC CTCCCGCGTT GCTCCCGGAA GCCCCGCCCCG

50

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human c-abl gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

GGGCGGGGCC TGGCGGGCGC CCTCTCCGGG CCCTTTGTTA ACAGGCGCGT

50

(2) INFORMATION FOR SEQ ID NO:378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human metallothionein-i-a gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

CGGCCCTCTT TCCCCTGACC ATAAAAGCAG CCGCTGGCTG CTGGGCCCTA

50

(2) INFORMATION FOR SEQ ID NO:379:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human metallothionein I-B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

ACCCACCCAC CTCCCCGAC TATAAAGGAG CAGCCAGCTC CTGGGCTCCA

50

(2) INFORMATION FOR SEQ ID NO:380:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human metallothionein-If (MT-IF)
gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

CCCGGCCCCC TCCCTGACT ATCAAAGCAG CGGCCGGCTG TTTGGGTCCA

50

(2) INFORMATION FOR SEQ ID NO:381:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene for 27 Kda heat shock
protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

CCCTCAAACG GGTCAATTGCC ATTAATAGAG ACCTCAAACA CCGCCTGCTA

50

(2) INFORMATION FOR SEQ ID NO:382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human 70 kDa heat shock protein gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

GCGGGTCTCC GTGACGACTT ATAAAACCCC AGGGGCAAGC GGTCCGGATA

50

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human macrophage alpha1-antitrypsin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

TGCCTCCACC CGAAGTCTAC TTCCTGGGTG GGCAGGAACT GGGCACTGTG

50

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human alphas-antitrypsin (S variant)
gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

CGTTGCCCCCT CTGGATCCAC TGCTTAAATA CGGACGAGGA CAGGGCCCTG

50

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human S variable segment 5' of
antithrombin III gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

TCTGCCCCAC CCTGTCTCTT GGAACCTCTG CGAGATTTAG AGGAAAGAAC

50

(2) INFORMATION FOR SEQ ID NO:386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human pulmonary surfactant protein
(SP5) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

CCCCTCTCCC TACGGACACA TATAAGACCC TGGTCACACC TGGGAGAGGA

50

(2) INFORMATION FOR SEQ ID NO:387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human Immunoglobulin kappa L-chain V
region gene (HK122)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

CCCCCTGCCC TGAAGACTTT TTATAGGCTG GTCACACCCG GAGCAGGAGT

50

(2) INFORMATION FOR SEQ ID NO:388:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human T cell receptor
V-alpha/J-alpha chain (rearranged)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

TTAAGGTTTG AATCCTCAGT GAACCAGGGC AGAAAAGAAT GATGAAATCC

50

(2) INFORMATION FOR SEQ ID NO:389:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene for HLA-DR alpha heavy
chain (class II antigen)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

TGCATTTTAA TGGTCAGACT CTATTACACC CCACATTCTC TTTTCTTTTA

50

(2) INFORMATION FOR SEQ ID NO:390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human MHC class IIHLA-DC-3-beta gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

CTACCACGCA TGGAAACATC CACAGATTTT TATTCTTTCT GCCAGGTACA

50

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human T-cell receptor CD3-gamma gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

GCCTTCTCTC AAAGGCCCCA GCCCAACAG TGATGGGTGG AGCCAGTCTA

50

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human pregnancy-specific beta-1 glycoprotein mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

CTGCCCTGGG AAGAGGCTCA GCACAGAAAG AGGAAGGACA GCACAGCTGA

50

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human pregnancy-specific
beta-1-glycoprotein 5 (PSG5)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

AGAGAGGAGG GGACAGAGAG GTGTCCTGGG CCTGACCCCA CCCATGAGCC

50

(2) INFORMATION FOR SEQ ID NO:394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human factor VIII gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

CCTGTGGCTG CTTCCCACTG ATAAAAAGGA AGCAATCCTA TCGGTTACTG

50

(2) INFORMATION FOR SEQ ID NO:395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

0123456789101112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899100

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human ubiquitin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

TGACGCAACA CTCGTTGCAT AAATTTCCT CCGCCAGCCC GGAGCATTTA

50

(2) INFORMATION FOR SEQ ID NO:396:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human proliferating cell nucleolar protein P120 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

ACTATAATAC GCCAAGCGTG CGTTCTGCCG TTCCCTCCGA CACGCGCGAC

50

(2) INFORMATION FOR SEQ ID NO:397:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene for delta-globin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

CAGGGAGGAC AGGACCAGCA TAAAAGGCAG GGCAGAGTCG ACTGTTGCTT

50

(2) INFORMATION FOR SEQ ID NO:398:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Gorilla fetal A-gamma-globin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

CGGCTGGCTA GGGATGAAGA ATAAAAGGAA GCACCCTCCA GCAGTTCCAC

50

(2) INFORMATION FOR SEQ ID NO:399:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene for fetal A-gamma and
G-gamma hemoglobin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

CGGCTGGCTA GGGATGAAGA ATAAAAGGAA GCACCCTTCA GCAGTTCCAC

50

(2) INFORMATION FOR SEQ ID NO:400:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Orangutan epsilon-globin gene with
flanking Alu repeats

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

CAGAACTTCG GCAGTGAAGA ATAAAAGGCC ACACAGAGAG GCAGCAGCAC

50

(2) INFORMATION FOR SEQ ID NO:401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human haptoglobin (Hpl) gene

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

TAAAAAGACC AGCAGATGCC CCACAGCACT GCTCTTCCAG AGGCAAGACC

50

- (2) INFORMATION FOR SEQ ID NO:402:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human low molecular weight oligoadenylate synthetase gene

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

AAGACAGCTC CTCCCTTCTG AGGAAACGAA ACCAACAGCA GTCCAAGCTC AGTCAGCAGA

60

AGAGATAAAA G

71

- (2) INFORMATION FOR SEQ ID NO:403:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human gene fragment for dihydrofolate reductase

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

GGGGGGCGGG GCCTCGCCTG CACAAATAGG GACGAGGGGG CGGGGCGGCC

50

(2) INFORMATION FOR SEQ ID NO:404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human thymidine kinase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

GGCTCGTGAT TGGCCAGCAC GCCGTGGTTT AAAGCGGTCG GCGCGGGACC

50

(2) INFORMATION FOR SEQ ID NO:405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human adenosine deaminase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

GCGGGAGGCG GGGCCCGGCC CGTTAAGAAG AGCGTGGCCG GCCGCGGCC

49

(2) INFORMATION FOR SEQ ID NO:406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human argininosuccinate synthase

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

TGCCCCCGGG CCCTGTGCTT ATAACCTGGG ATGGGCACCC CTGCCAGTCC

50

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human ornithine aminotransferase
gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

GGGGGCGGGG CAGAATCAGC CTTAAGTTG CAGTGACGCT CCGGCGTCAC

50

(2) INFORMATION FOR SEQ ID NO:408:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human tyrosine hydroxylase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

TGACGTCAGC TCAGCTTATA AGAGGCTGCT GGGCCAGGGC TGTGG

45

(2) INFORMATION FOR SEQ ID NO:409:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human HMG CoA reductase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

CAGCTCCGAG CGTGCCTAAG GTGAGGGCTC CTTCCGCTCC GCGACTGCGT

50

(2) INFORMATION FOR SEQ ID NO:410:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene for lecithin-cholesterol
acyltransferase

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

CCTAGGGCCC CTCCCACTCC CACACCAGAT AAGGACAGCC CAGTGCCGCT

50

(2) INFORMATION FOR SEQ ID NO:411:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human porphobilinogen deaminase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

CGCCCAGAGG GAGGGACCTC CCCTTCGAGG GAGGGCGCCG GAAGTGACGC

50

(2) INFORMATION FOR SEQ ID NO:412:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human porphobilinogen deaminase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

GCACAGCACT CCCACTGACA ACTGCCTTGG TCAAGGTGGG CTTCAGGGCT

50

(2) INFORMATION FOR SEQ ID NO:413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human URO-D gene for
uroporphyrinogen decarboxylase

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

GGGGGGCAGG CTCAGATTCA GGTAAATTG TGGATTGAGC TCGCAGTTAC

50

(2) INFORMATION FOR SEQ ID NO:414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human URO-D gene for
uroporphyrinogen decarboxylase

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

GGGGGGCAGG CTCAGATTCA GGTAAATTG TGGATTGAGC TCGCAGTTAC A

51

(2) INFORMATION FOR SEQ ID NO:415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human aldolase B (ALDOB) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

AAAAAAAAA CATGATGAGA AGTCTATAAA AATTGTGTGC TACCAAAGAT

50

(2) INFORMATION FOR SEQ ID NO:416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human aldolase A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

GGTGGCGCTG CTCACCACAC ACAAGTGTTA TAGGAGGAGT CTGGCCCTTG

50

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human aldolase A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

GGTGGCGCTG CTCACCACAC ACAAGTGTTA TAGGAGGAGT CTGGCCCTTG A

51

(2) INFORMATION FOR SEQ ID NO:418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human aldolase A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

TGTGGGGCGG GCAGGAGCTG CCTTATAACC AGCCCGGGAA CCCCTAGCTC

50

(2) INFORMATION FOR SEQ ID NO:419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human aldolase A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

TGTGGGGCGG GCAGGAGCTG CCTTATAACC AGCCCGGGAA CCCCTAGCTC A

51

(2) INFORMATION FOR SEQ ID NO:420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human aldolase A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

GCTCGGCGGA GGGCGGAGTG GTGCCTTTAA AAGGCCGGGC GCCGCCTTCC

50

(2) INFORMATION FOR SEQ ID NO:421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human aldolase A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

GCTCGGCGGA GGGCGGAGTG GTGCCTTTAA AAGGCCGGGC GCCGCCTTCC G

51

(2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human aldolase A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

GCTAAATCGG CTGCGTTCCT CTCGGAACGC GCCGCAGAAG GGGTCCTGGT

50

(2) INFORMATION FOR SEQ ID NO:423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human aldolase A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

GCTAAATCGG CTGCGTTCCT CTCGGAACGC GCCGCAGAAG GGGTCCTGGT G

51

(2) INFORMATION FOR SEQ ID NO:424:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human phosphoglycerate kinase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

GAGGCGGGGT GTGGGGCGGT AGTGTGGGCC CTGTTCTGTC CCGCGCGGTG

50

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene for glucose 6-phosphate
dehydrogenase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

CAGGCGCCCG CCCCCGCCCC CGCCGATTAA ATGGGCCGGC GGGGCTCAGC

50

(2) INFORMATION FOR SEQ ID NO:426:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human hepatic lipase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

GCAGTCTTCC CTAACAAAGT ATCTAATAGG CATTGTGGTC TCTTTGGCTT

50

(2) INFORMATION FOR SEQ ID NO:427:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human hepatic lipase mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

GCAGTCTTCC CTAACAAAGT ATCTAATAGG CATTGTGGTC TCTTTGGCTT C

51

(2) INFORMATION FOR SEQ ID NO:428:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human protein C gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

AGTGCTGAGG GCCAAGCAA TATTTGTGGT TATGGATTAA CTCGAACTCC

50

(2) INFORMATION FOR SEQ ID NO:429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human factor IX gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

CCAGAAGTAA ATACAGCTCA GCTTGTACTT TGGTACAACT AATCGACCTT

50

(2) INFORMATION FOR SEQ ID NO:430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human MHC III HLA factor B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

GCAGGTGCCA GAACACAGAT TGTATAAAAG GCTGGGGGCT GGTGGGGAGC

50

(2) INFORMATION FOR SEQ ID NO:431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human pepsinogen gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

CGATAAGGCG GGACCCAACT TGTATATAAG GGCAGCTCAT GCTGCTGCTC

50

246

(2) INFORMATION FOR SEQ ID NO:432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human pepsinogen C gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

CGATTAGACT AATCTTGGGC GTATAAAGA GGAAAGAGTG CCCAGGTCTT

50

(2) INFORMATION FOR SEQ ID NO:433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human collagenase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

CTGGAAGGGC AAGGACTCTA TATATACAGA GGGAGCTTCC TAGCTGGGAT

50

(2) INFORMATION FOR SEQ ID NO:434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human stromelysin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

CCAAACAAAC ACTGTCACCTC TTAAAAAGCT GCGCTCCCGA GGTGGACCT

50

(2) INFORMATION FOR SEQ ID NO:435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human alpha-amylase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

TCTGATCCGT GCAGGGTATT AATGTGTCAG GGCTGAGTGT TCTGAGATTT

50

(2) INFORMATION FOR SEQ ID NO:436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human pancreatic alpha-amylase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

TGTAATATGT GCTTCTTACA GGAATATAAA TAGTTTCTGG AAAGGACACT

50

(2) INFORMATION FOR SEQ ID NO:437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human pancreatic amylase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

TGTAAAATGT GCTTCTTACA GGAATATAAA TAGTTTCTGG AAAGGACACT

50

(2) INFORMATION FOR SEQ ID NO:438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: human cytochrome P450c gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

GCCACACGTA CAAGCCCGCC TATAAAGGTG GCAGTGCCTT CACCCTCACC

50

(2) INFORMATION FOR SEQ ID NO:439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human cytochrome P-450c gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

GCCACACGTA CAAGCCCGCC TATAAAGGTG GCAGTGCCTT CACCCTCACC C

51

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene for cytochrome P(1)-450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

CACGTACAAG CCCGCCTATA AAGGTGGCAG TGCCTTCACC

40

(2) INFORMATION FOR SEQ ID NO:441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human steroid 21-hydroxylase [P450 (C21)] B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

GGATGGCTGG GGCTCTTGAG CTATAAGTGG CACCTCAGGG CCCTGACGGG

50

(2) INFORMATION FOR SEQ ID NO:442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human mitochondrial aldehyde dehydrogenase 2 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

TTCCTGACCA TGGTACTTAT AAAAGCAGTG CCGTCTGCCC CATCCATGTC

50

(2) INFORMATION FOR SEQ ID NO:443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human carbonic anhydrase III gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

AAGGCCATGC AAGTGTGCGG GGGAGCTACA TAAAAGCGCG GGCTCGCGCG

50

(2) INFORMATION FOR SEQ ID NO:444:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human creatine kinase B isozyme gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

TGGGCGGCCC GCGTTGTGCC CCTTAAGAGC CGCGGGAGCG CGGAGCGGCC

50

(2) INFORMATION FOR SEQ ID NO:445:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human preproenkephalin A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

CTTCGGTTTG GGGCTAATTA TAAAGTGGCT CCAGCAGCCG TTAAGCCCCG

50

(2) INFORMATION FOR SEQ ID NO:446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human preprokephalin A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

CTTCGGTTTG GGGCTAATTA TAAAGTGGCT CCAGCAGCCG TTAAGCCCCG G

51

(2) INFORMATION FOR SEQ ID NO:447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human prepro form of corticotropin releasing factor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

TTTTTGAAGA GGGTCGACAC TATAAAATCC CACTCCAGGC TCTGGAGTGG

50

(2) INFORMATION FOR SEQ ID NO:448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human preprothyrotropin-releasing hormone gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

GACCTCACTC GAGCCGCCGC CTGGCGCAGA TATAAGCGGC GGCCCATCTG

50

(2) INFORMATION FOR SEQ ID NO:449:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human gene for fetal A-gamma and G-gamma hemoglobin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

CGGCTGGCTA GGGATGAAGA ATAAAAGGAA GCACCCTTCA GCAGTTCCAC

50

(2) INFORMATION FOR SEQ ID NO:450:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Human gene coding for ACTH and beta-LPH precursors

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

CCCACCAGGA GAGCTCGGCA AGTATATAAG GACAGAGGAG CGCGGGACCA

50

(2) INFORMATION FOR SEQ ID NO:451:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human somatostatin I gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

TAGCCTGACG TCAGAGAGAG AGTTTAAAAC AGAGGGAGAC GGTGAGAGC

50

(2) INFORMATION FOR SEQ ID NO:452:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human glucagon gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

GTGAGGCTAA ACAGAGCTGG AGAGTATATA AAAGCAGTGC GCCTTGGTGC

50

(2) INFORMATION FOR SEQ ID NO:453:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human glucagon gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

GTGAGGCTAA ACAGAGCTGG AGAGTATATA AAAGCAGTGC GCCTTGGTGC A

51

(2) INFORMATION FOR SEQ ID NO:454:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human chorionic gonadotropin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

AGGTGGAAC ACTCTGCTGG TATAAAGCA GGTGAGGACT TCATTAAGT

50

(2) INFORMATION FOR SEQ ID NO:455:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human chorionic gonadotropin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

TTGAAGTGTG GTGCAGGAAA GCCTCAAGTA GAGGAGGGTT GAGGCTTCAA

50

(2) INFORMATION FOR SEQ ID NO:456:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human beta-LH gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

GCCGCCCCCA CAACCCCGAG GTATAAAGCC AGATACACGA GGCAGGGGAT

50

(2) INFORMATION FOR SEQ ID NO:457:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human follicle-stimulating hormone
beta-subunit gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

TAGTTGCACA TGATTTTGTA TAAAAGGTGA ACTGAGATT CATTCACTCT

50

(2) INFORMATION FOR SEQ ID NO:458:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human prolactin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

TATTCATGAA GATATCAAAG GTTTATAAAG CCAATATCTG GGAAAGAGAA

50

(2) INFORMATION FOR SEQ ID NO:459:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human parathyroid gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

GACATCATCT GTAACAATAA AAGAGCCTCT CTTGGTAAGC AGAAGACCTA

50

(2) INFORMATION FOR SEQ ID NO:460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Owl monkey insulin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

GGGGAGATGG GCTCTGGGCC TATAAAGCCA GCAGGGACCC AGCAGCCCTC

50

(2) INFORMATION FOR SEQ ID NO:461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: human insulin/IGF II gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

CCCCGCCTCC AGAGTGGGGG CCAAGGCTGG GCAGGCGGGT GGACGGCCGG

50

(2) INFORMATION FOR SEQ ID NO:462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human insulin like growth factor
IGFII gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

AAAGAACTCT GCCTTGCGTT CCCAAAATT TGGGCATTGT TCCGGCTCGC

50

(2) INFORMATION FOR SEQ ID NO:463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human insulin-like growth factor II gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

CCCTGGGCCG CGGCTGGCGC GACTATAAGA GCCGGGCGTG GGCGCCCGCA

50

(2) INFORMATION FOR SEQ ID NO:464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human gastrin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

AGTTGGGAGG GACCTTGAGG GCTTTATAAG GCAGGCCTGG AGCATCAAGC

50

(2) INFORMATION FOR SEQ ID NO:465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human interferon alpha gene
INF-alpha 13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

GGAAATCAGT ATGTTCCCTA TTTAAGGCAT CTGCAGGAAG CAAAGCCTTC

50

(2) INFORMATION FOR SEQ ID NO:466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene for leukocyte interferon

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

GGAAGCTAGT ATGTTCCCTA TTTAAGACCT ATGCACAGAG CAAGGTCTTC

50

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human interferon alpha gene
INF-alpha 4b

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

GGAAATTAGT ATGTTCACTA TTTAAGACCT ATGCACAGAG CAAAGTCTTC

50

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene for leukocyte (alpha) interferon

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

GGAAATTAGT ATGTTCACTA TTTAAGGCCT ATGCACAGAG CAAAGTCTTC

50

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human interferon genes LeIF-L and LeIF-J

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

GGAAATTAGT ATGTTCACTA TTTAAGACCT ATGCACAGAG CAAAGTCTTC

50

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene for fibroblast (beta-1) interferon

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

ATAGAGAGAG GACCATCTCA TATAAATAGG CCATACCCAC GGAGAAAGGA

50

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human c-sis gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

CTCTCGCACT CTCCCTTCTC CTTTATAAAG GCCGGAACAG CTGAAAGGGT

50

(2) INFORMATION FOR SEQ ID NO:472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human migratory inhibitory
factor-related protein 8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

CAGCTGGCCA AGCCTAACCG CTATAAAAAG GAGCTGCCTC TCAGCCCTGC

50

(2) INFORMATION FOR SEQ ID NO:473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human migratory inhibitory
factor-related protein 14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

GTGCCCCAGT CAGGAGCTGC CTATAAATGC CGAGCCTGCA CAGCTCTGGC

50

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human epidermal growth factor related gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

GGTCCCTCCT CCTCCGCCC TGCCTCCCGC GCCTCGGCC GCGCGAGCTA

50

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human opsin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

GCTTAGGAGG GGGAGGTCAC TTTATAAGGG TCTGGGGGGG TCAGAACCCA

50

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human blue cone photoreceptor pigment gene

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

TTTTGTGGGG TGGGAGGATC ACCTATAAGA GGA CTCAGAG GAGGGTGTGG

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(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human red cone photoreceptor pigment gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

CGGGCTGATC CCACAGGCCA GTATAAAGCG CCGTGACCCT CAGGTGATGC

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(2) INFORMATION FOR SEQ ID NO:478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human green cone photoreceptor pigment gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

CGGGCTGATC CCACTGGCCG GTATAAAGCG CCGTGACCCT CAGGTGACGC

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(2) INFORMATION FOR SEQ ID NO:479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human interferon-inducible gene
IFI-56K

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

TTGGCTGCTG TTTAGCTCCC TTATATAACA CTGTCTTGGG GTTTAAACGT

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(2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human interferon-induced 15-Kd
protein (ISG) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

GACGTGTGTG CCTCAGGCTT AATAATAGGG CCGGTGCTGC TGC GGAAGCC

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(2) INFORMATION FOR SEQ ID NO:481:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human ubiquitin-like protein (GdX)
gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

TCCAGCGCGC GCGCCCGGGG CGGCGGCGCG CGGCGGGGGG TGGTTGGGGT

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(2) INFORMATION FOR SEQ ID NO:482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human exogenous retrovirus erv3 5" long terminal repeat

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

CCGCCCCTGT TGGTTGCATG TATAAAAGTC AAGCCCTGTC ATTGTTTCAGG

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(2) INFORMATION FOR SEQ ID NO:483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Bovine leukemia virus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

ACCTCACCTG CTGATAAATT AATAAAATGC CGGCCCTGTC GAGTTAGCGG

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(2) INFORMATION FOR SEQ ID NO:484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human T-cell lymphotropic virus type I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

TCAATAAACT AGCAGGAGTC TATAAAAGCG TGGAGACAGT TCAGGAGGGG

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(2) INFORMATION FOR SEQ ID NO:485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human T-cell leukemia virus II proviral LTR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

TCAAAATAAA AGATGCCGAG TCTATAAAAG CGCAAGGACA GTTCAGGAGG

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(2) INFORMATION FOR SEQ ID NO:486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human T-cell Lymphotropic virus type III (HIV-1)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

GGCGAGCCCT CAGATCCTGC ATATAAGCAG CTGCTTTTTG CCTGTACTGG

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(2) INFORMATION FOR SEQ ID NO:487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Aids-associated retrovirus (arv-2;proviral)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

TGGCGTCCCT CAGATGCTGC ATATAAGCAG CTGCTTTTTG CCTGTACTGG

50

(2) INFORMATION FOR SEQ ID NO:488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human immunodeficiency virus type 2 (HIV-2)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

GCCCTCATAT TCTCTGTATA AATATACCCG CTAGCTTGCA TTGTACTTCG

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(2) INFORMATION FOR SEQ ID NO:489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Visna lentivirus, Icelandic strains LV1-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

CATAACCGCA GATGTAAACA AGTTGCCTAT ATAAGCCGCT TGCTAGCTGG

50

(2) INFORMATION FOR SEQ ID NO:490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human cytomegalovirus strain AD169
gene I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

GGCGTGTACG GTGGGAGGTC TATATAAGCA GAGCTCGTTT AGTGAACCGT

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(2) INFORMATION FOR SEQ ID NO:491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Murine cytomegalovirus
intermediate-early gene I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

GCTGAGCTGC GTTCACGTGG GTATAAGAGG CGCGACCAGC GTCGGTACCG

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(2) INFORMATION FOR SEQ ID NO:492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human cytomegalovirus
intermediate-early glycoprotein UL37

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

CGTCATGTCC GGCATCTTCA TGTATATAAG ACGGTGTTTC AAGACGACGT

50

(2) INFORMATION FOR SEQ ID NO:493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human cytomegalovirus I-E
glycoprotein US3 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

ACAACGTCAC CAAGAAACGC TATATATTCA AAAACACCGT TCAGTCCACA

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(2) INFORMATION FOR SEQ ID NO:494:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Herpes Simplex Virus type 1 gene I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

TTTGGGGAGG GGAAAGGCGT GGGGTATAAG TTAGCCCTGG CCCGACAGTC

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(2) INFORMATION FOR SEQ ID NO:495:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Herpes Simplex Virus type 1 gene II

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

AGCCGGCCCC GGCACCACGG GTATAAGGAC ATCCACCACC CGGCCGGTGG

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(2) INFORMATION FOR SEQ ID NO:496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Herpes simplex virus type II I-E
gene II

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

AGCCGGCCCC GTCGTGCGG GTATAAGGGC AGCCACCGGC CCACTGGGCG

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(2) INFORMATION FOR SEQ ID NO:497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Herpes simplex virus type I I-E gene
III

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

TTCCCGCCGG CCCCTGGGAC TATATGAGCC CGAGGACGCC CCGATCGTCC

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(2) INFORMATION FOR SEQ ID NO:498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Herpes simplex virus type II I-E
gene III

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

CCCCGCGCGC CCCGAGCGAC TATATCAGCC AGGCGACGGG GCGATCGTCC

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(2) INFORMATION FOR SEQ ID NO:499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Herpes simplex virus type 1 I-E
genes IV and V

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

GGGGGCGGGT CTCTCCGGCG CACATAAAGG CCCGGCGCGA CCGACGCCCC

50

(2) INFORMATION FOR SEQ ID NO:500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Herpes simplex virus type 2 I-E
genes IV and V

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

ACGGGGGGCG GGCCGTTCTT CGCGCACATA AAGGGCCGGC GTCCCGGTCG

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(2) INFORMATION FOR SEQ ID NO:501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human cytomegalovirus DNA
polymerase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

TAGGCGGGCT GGAAAGATGA TGTATAAATA GAGTCTGCGA CGGGGTTCGG

50

(2) INFORMATION FOR SEQ ID NO:502:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human cytomegalovirus b' 2.2 kb
transcript (start 160513)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:

TAGGCGGGCT GGAAAGATGA TGTATAAATA GAGTCTGCGA CGGGGTTCGG

50

(2) INFORMATION FOR SEQ ID NO:503:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human cytomegalovirus 2.7 kb
transcript (start 4578)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

GCCCGCGCTC GGCAGAGCTA CCATATAAAA ACGCAGGGGT TTAGCAGCTT

50

(2) INFORMATION FOR SEQ ID NO:504:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b' 82K AlkExo
(start 27048)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:

CAGCACCAGG AGAGGCTTAA GCTCGGGAGG CAGCGCCACC GACGACAGTA

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(2) INFORMATION FOR SEQ ID NO:505:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b' 42K gene
(start site 106547)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

ATGGGTTGTG GTTATATGCA CTTCTATAA GACTCTCCCC CACCGCCCAC

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(2) INFORMATION FOR SEQ ID NO:506:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 39k dUTPase
gene (start 106811)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

CGTGTGCGAT AATACACACG CCCATCGAGG CCATGCCTAC ATAAAAGGGC

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(2) INFORMATION FOR SEQ ID NO:507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b' 33K (start site 145165)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

GGCCGGGCGA CCCAGATGTT TACTTAAAAG GCGTGCCGTC CGCCGGCATG

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(2) INFORMATION FOR SEQ ID NO:508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 21K (start site 145459)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

CGACGTACGC GATGAGATCA ATAAAAGGGG GCGTGAGGAC CGGGAGGCGG

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(2) INFORMATION FOR SEQ ID NO:509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b' 5 kb transcript (start 86216)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

CCCCACCCCT GCGCGATGTG GATAAAAAGC CAGCGCGGGT GGTTTAGGGT

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(2) INFORMATION FOR SEQ ID NO:510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b' RNR2 gene
(start 89774)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

GGTCCGCCTT CTGGTCCACG CATATAAGCG CGGACTAAAA ACAGGGATGT

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(2) INFORMATION FOR SEQ ID NO:511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Herpes simplex virus-2 RNR2 gene
(start site 247)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:

TGGTCCGCCT TCTCGTCCAC GCATATAAGC GCGGCCTGAA GACGGGGATG

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(2) INFORMATION FOR SEQ ID NO:512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b' tk gene
(start site 47911)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:

CGCGGTCCCA GGTCCACTTC GCATATTAAG GTGACGCGTG TGGCCTCGAA

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(2) INFORMATION FOR SEQ ID NO:513:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Herpes simplex virus-2 b' tk gene
(start site 225)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

CGCGGCCCGA GGTCCACTTC GCATATTAAG GTGACGCGCG TGGCCTCGAA

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(2) INFORMATION FOR SEQ ID NO:514:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b' dbp gene
(start site 62318)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

CGGCACGCCC CCAGGTAAAG TGTACATATA CCAACCGCAT ACCAGACGCA

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(2) INFORMATION FOR SEQ ID NO:515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b' gB (3.3 Kb) start 56081

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

CCACTCAGCG CGCCGCCTGG CGATATATTC GCGAGCTGAT TATCGCCACC

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(2) INFORMATION FOR SEQ ID NO:516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b' gD (start 138337)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

CCACTCAGCG CGCCGCCTGG CGATATATTC GCGAGCTGAT TATCGCCACC

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(2) INFORMATION FOR SEQ ID NO:517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Herpes simplex virus-2 b' gD (start 5918)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

GGAGTATAAT AGAGTCTTTG TGTTTAAAAC CCGGGGTCGG TGTGGTGTTC

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(2) INFORMATION FOR SEQ ID NO:518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b' gE (start site 141171)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

GGAGAGGGCC CGCGGCGCAT TTAAGGCGTT GTTGTGTTGA CTTTGCCTCT

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(2) INFORMATION FOR SEQ ID NO:519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 ICP gene (start site 58361)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

AATTATTGCT ACGACATCCG TGCTTGTTTG TGTTCCGTGT CTATATCTCT

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(2) INFORMATION FOR SEQ ID NO:520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b' tr-4
(start site 136729)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

GGCGGTGCTG TTTGCGGGTT GGCACAAAAA GACCCCGATC CGCGTCTGTG

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(2) INFORMATION FOR SEQ ID NO:521:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 [U-S] b' tr-9
(start 143245)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

GTGACGTCAA TTGCCCGAGG CGCATAAAGG GCCGGTGGTC CGCCTAGCCG

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(2) INFORMATION FOR SEQ ID NO:522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b'g' VP5
(start 40768)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:

GGGGTGGGGC GGGGGGGGGG GTATATAAGG CCTGGGATCC CACGTCCCCG

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(2) INFORMATION FOR SEQ ID NO:523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b'g' 2.1kb
transcript (start 26639)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:

CCCGTTAACC CCCCACGTGA TCAGCACGCC ACCGACACCG CAGACGAAAA

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(2) INFORMATION FOR SEQ ID NO:524:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b'g'
a'TIF/VSP (start 105259)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

GGGGCGGCCC GTGCGGGTTG CTAAATGCG TGGTGGCGAC CACGGGCTGT

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(2) INFORMATION FOR SEQ ID NO:525:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b'g' 2.7 kb
transcript (start 100998)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

GCCACGCCCA TAAGCTCCTC CCGATAAAAA GCGCCCCGAT GGCCCTGGAC

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(2) INFORMATION FOR SEQ ID NO:526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human cytomegalovirus UL36 gene
(start 49862)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:

GACGTCAACG CTGATAGTGT CTATAAAGGC CGTGCCGCCG CGCCGTAGTT

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(2) INFORMATION FOR SEQ ID NO:527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human cytomegalovirus g' pp65 gene
(start 121072)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

TCCGCGTTTG GTCGCCTGCC TATGTAAGGC GGCGGCCGCA GAGGGCGCGC

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(2) INFORMATION FOR SEQ ID NO:528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human cytomegalovirus g' pp71 gene
(start 119223)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

GTCACCGCTG CTATATTTGC GACAGTTGCC GGAACCCTTC CCGACCTCCC

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(2) INFORMATION FOR SEQ ID NO:529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human cytomegalovirus g' pp150 gene
(start 43092)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

CGTATCCGCC TCCGCTATTA AACTACCCCC CCTCCCTCTA GGTGGGGCGC

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(2) INFORMATION FOR SEQ ID NO:530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 g' 5 Kb
transcript (start 103313)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

TTGTGTCGCA GGGCGGCCCG CGTATAAAGG CGAGAGCGCG GGACCGTTTC

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(2) INFORMATION FOR SEQ ID NO:531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 g' gC (start 96170)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

AACCCCGGAT GGGGCCCGGG TATAAATTCC GGAAGGGGAC ACGGGCTACC

50

(2) INFORMATION FOR SEQ ID NO:532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Herpes simplex virus-2 g' gC (start 670)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

GCGGGGGTGC CGTGGACGGG TATAAAGGCC AGGGGGGCAC GCGGGCCCAT

50

(2) INFORMATION FOR SEQ ID NO:533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 g' gH gene (start 46581)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

CGGCAATAAA AAGACAGAAT AAAACGCACG GGTGTTGGGT CGTTTGTTC

50

(2) INFORMATION FOR SEQ ID NO:534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 g' 42 K
(start site 107130)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:

CCGAGATCCC CGCTAACCTT CGGCATAAAA GCCACCGCGC GCCTGTTGAC

50

(2) INFORMATION FOR SEQ ID NO:535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 Ori_s ORF
(start site 132287)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:

CGGAGGCCCC CGGGGTGCGT CCCCTGTGTT TCGTGGGTGG GGTGGGCGGG

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(2) INFORMATION FOR SEQ ID NO:536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 18 K (start
site 97951)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:

CCCGCCCACC GCTGGGCGCT ATAAAGCCGC CACCCTCTCT TCCCTCAGGT

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(2) INFORMATION FOR SEQ ID NO:537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Herpes simplex virus-2 18K (start site 2391)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:

CCCCGCCGTC CCCCAGGCGT TATAAGCCGC CGCACTCGCT TTTCCCACCG

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(2) INFORMATION FOR SEQ ID NO:538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Epstein Barr virus L1 1Kb gene (start site 103194)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:

TGGTGCCTTG GCTTTAAAGG GGAGATGTTA GACAGGTAAC TCACTAAACA

50

(2) INFORMATION FOR SEQ ID NO:539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

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(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Epstein Barr virus R1 145K gene
(start site 1721)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

ACTGTATAAA GGTAAGTATT ATTAAATTTT AGAGACACTA TCACGTGTAA

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(2) INFORMATION FOR SEQ ID NO:540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Epstein Barr virus R1 20K (start
site 9660)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

CTTTTAGCCA TGCCATGCTC TATAAATCAC TTCCCTATCT CAGGTAGGCC

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(2) INFORMATION FOR SEQ ID NO:541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Epstein Barr virus [DL/R] (start
site 52787)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:

ACAGAGACCC CAAAAGAGG ATAAAAGAAG GCGAGCCGGC CCGGCTCGCC

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(2) INFORMATION FOR SEQ ID NO:542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Epstein Barr virus R2 (start site 61372)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:

GTGACGGTCA GGCAGCTCCT GTATTTAACT TTGCGGACAG AGGCCAGAGC

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(2) INFORMATION FOR SEQ ID NO:543:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Epstein Barr virus L2 (start site 57050)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:

TAATTACGCT TGTGTACATA TTAAATCCA CACAAGTGGC CAGAGTGGGC

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(2) INFORMATION FOR SEQ ID NO:544:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Epstein Barr virus R1 (start site 88539)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:

GACAGGGACG GCGGCGCTAT ATATAAGAGC CCAAGACCCG GCTCTCTTTA

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(2) INFORMATION FOR SEQ ID NO:545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Epstein Barr virus R2 (start site 88897)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:

CGGATTAGAT GGGGATATTT AAAAGGGGCA GCAATCTCGG CTGTTTGTAC

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(2) INFORMATION FOR SEQ ID NO:546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Epstein Barr virus L2 (start site 90021)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

ACCCAACAGG TGGTGAAAT ATAACACAGG TGACACCAGC CTCTATCAGC

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(2) INFORMATION FOR SEQ ID NO:547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Epstein Barr virus [BamH1-L] L1 (start site 92157)

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(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Epstein Barr virus [BamH1-K] 1.3kb
transcript (start 110632)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:

TTGCGACCCC TCTGATATTA AGGTGGTTAT TTTGGGCCAG GACCCCTATC

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(2) INFORMATION FOR SEQ ID NO:551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Epstein Barr virus [EcoR1-H] L1
(start site 137680)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:

CGGTGCCCCG ACTCAGAATT ATTAAACCGG GTGGCAGCTC CTGGCAGTCA

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(2) INFORMATION FOR SEQ ID NO:552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Epstein Barr virus [EcoR1-D] L1
(start site 159337)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:

AAGGGCAGGG GGTGGGTATT TAAGGATCTA TATGCCCTTC TCTACCTGCA

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(2) INFORMATION FOR SEQ ID NO:553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Epstein Barr virus [EcoR1-D] R1
(start 165496)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:

AATGGGCGTG GCAGAATAGT ATAAGACGCG AGGCCTGGGT GAGGAGAGTC

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(2) INFORMATION FOR SEQ ID NO:554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Epstein Barr virus [EcoR1-D] L2
(start 167495)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:

TCTTTCCTTG TCCTTACTGT ATAAAAGTCC ACGAAAACAG CTGTGCCTCA

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(2) INFORMATION FOR SEQ ID NO:555:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Epstein Barr Virus [EcoR1-D] L1A
start 169165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:

ACTGATGAGT AAGTATTACA CCCTTTGCCC CACACCCCCT TTCCCTTACT

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(2) INFORMATION FOR SEQ ID NO:556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Epstein Barr Virus [EBNA] E1 (start site 11333)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:

AGGGGGGGGAC TAAGGTCCCA CTACAAAAC TCTGTGTTCT GCTGCAAATT

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(2) INFORMATION FOR SEQ ID NO:557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Epstein Barr virus [EBNA] E2 (start site 14399)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:

GGTATAAAGT GGTCTGCAG CTATTTCTGG TCGCATCAGA GCGCCAGGAG

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(2) INFORMATION FOR SEQ ID NO:558:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Epstein Barr virus [EcoR1-D] L1
(start site 169514)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:

CTCTGACGTA GCCGCCCTAC ATAAGCCTCT CACACTGCTC TGCCCCCTTC

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(2) INFORMATION FOR SEQ ID NO:559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Adenovirus type 2 E1a (start 498)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:

GTCAGCTGAC GCGCAGTGTA TTTATACCCG GTGAGTTCCT CAAGAGGCCA

50

(2) INFORMATION FOR SEQ ID NO:560:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Adenovirus type-5 E1a (start 499)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:

GTCAGCTGAC GTGTAGTGTA TTTATACCCG GTGAGTTCCT CAAGAGGCCA

50

(2) INFORMATION FOR SEQ ID NO:561:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Adenovirus type-7 EIa (start site 512)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:

TCAGCTGATC GCTAGGGTAT TTAAACCTGA CGAGTTCCGT CAAGAGGCCA

50

(2) INFORMATION FOR SEQ ID NO:562:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Adenovirus type-12 Ela (start site 306)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:

AAATTGATGA CGGCAATTTT ATTATAGGCG CGGAATATTT ACCGAGGGCA

50

(2) INFORMATION FOR SEQ ID NO:563:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Adenovirus type-12 EIa (start site 445)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:

GTCAGCTGAT CGTTTGGGTA TTTAATGCCG CCGTGTTCGT CAAGAGGCCA

50

(2) INFORMATION FOR SEQ ID NO:564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Simian Adenovirus SA7 E1a (start site 440)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:

TTATTGTCTA GGTGAGGGTA TTAAACCGG CTCAGACCGT CAAGAGGCCA

50

(2) INFORMATION FOR SEQ ID NO:565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Adenovirus type-2 E1b (start 1700)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:565:

GGGGCGGGGC TTAAAGGGTA TATAATGCGC CGTGGGCTAA TCTTGGTTAC

50

(2) INFORMATION FOR SEQ ID NO:566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Adenovirus type-5 E1b (start site 1703)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:

GGGGCGGGGC TTAAAGGGTA TATAATGCGC CGTGGGCTAA TCTTGGTTAC

50

(2) INFORMATION FOR SEQ ID NO:567:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Adenovirus type-7 E1b (start site 1577)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:

TTCTTGGGTG GGGTCTTGGA TATATAAGTA GGAGCAGATC TGTGTGGTTA

50

(2) INFORMATION FOR SEQ ID NO:568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Adenovirus type-12 E1b (start site 1527)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:

TGGGCGTGGT TAAACAGGGA TATAAAGCTG GGTGGTGTT GCTTTGAATA

50

(2) INFORMATION FOR SEQ ID NO:569:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Adenovirus type-2 EII (start site 27092)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:

GAAAGGGCGC GAAACTAGTC CTTAAGAGTC AGCGCGCAGT ATTTGCTGAA

50

(2) INFORMATION FOR SEQ ID NO:570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Adenovirus type-2 EIII (start site 27610)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:

TGCGGTCGCC CGGGCAGGGT ATAAC TCACC TGAAAATCAG AGGGCGAGGT

50

(2) INFORMATION FOR SEQ ID NO:571:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Adenovirus type-5 EIII (start site 239)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:

TGCGGTCGCC CGGGCAGGGT ATAAC TCACC TGACTCTTGG AGGGCGAGGT

50

(2) INFORMATION FOR SEQ ID NO:572:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Adenovirus type-2 EIV (start site 35611)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:

TTACGTCATT TTTTAGTCCT ATATATACTC GCTCTGTACT TGGCCCTTTT

50

(2) INFORMATION FOR SEQ ID NO:573:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Adenovirus type-2 IVa2 (start site 5827)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:

CCCTCCCACT TAGCCTCCTT CGTGCTGGCC TGGACGCGAG CCTTCGTCTC

50

(2) INFORMATION FOR SEQ ID NO:574:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Adenovirus type-5 IVa2 (start site 5837)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:

CCCTCCCACT TAGCCTCCTT CGTGCTGGCC TGGACGCGAG CCTTTGTCTC

50

(2) INFORMATION FOR SEQ ID NO:575:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Adenovirus type-7 IVa2 (start site 5692)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:

CCCTCCCACG TGGCCTCCTT TGTGCTGGCC TGGACACGCG CTTTGTATC

50

(2) INFORMATION FOR SEQ ID NO:576:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Adenovirus type-2 IX (start site 3575)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:

GCTTAAGGGT GGGAAAGAAT ATATAAGGTG GGGGTCTCAT GTAGTTTTGT

50

(2) INFORMATION FOR SEQ ID NO:577:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Adenovirus type-5 IX (start site 3581)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:

GCTTAAGGGT GGGAAAGAAT ATATAAGGTG GGGGTCTTAT GTAGTTTGT

50

(2) INFORMATION FOR SEQ ID NO:578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Adenovirus type-7 IX (start site 3460)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:

ATGGGGACTT TCAGGTTGGT AAGGTGGACA AATTGGGTAA ATTTTGTAA

50

(2) INFORMATION FOR SEQ ID NO:579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Adenovirus type-2 major late (start site 6039)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

GTGTTCTGA AGGGGGGCTA TAAAAGGGGG TGGGGGCGCG TTCGTCCTCA

50

(2) INFORMATION FOR SEQ ID NO:580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Adenovirus type-5 major late (start site 6049)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:

GTGTTCTGA AGGGGGGCTA TAAAAGGGGG TGGGGGCGCG TTCGTCCTCA

50

(2) INFORMATION FOR SEQ ID NO:581:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Adenovirus type-7 major late (start site 5904)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:

GGGTCCCCGC CGGGGGGGTA TAAAAGGGGG CGGACCTCTG TTCGTCCTCA

50

(2) INFORMATION FOR SEQ ID NO:582:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Adenovirus type-12 major late (start site 972)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:

AATTTTCTGG TGGTGGGCTA TAAAAGGGG CGGGTCCTTG GTCTTCATCG

50

(2) INFORMATION FOR SEQ ID NO:583:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Adenovirus type-2 LIIa (start site 25954)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:

GGCGTGGTAG TCCTCAGGTA CAAATTGCG AAGGTAAGCC GACGTCCACA

50

(2) INFORMATION FOR SEQ ID NO:584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human papilloma virus type 18 E6 gene (start site 30)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:

CAGCACATAC TATACTTTTC ATTAATACTT TTAACAATTG TAGTATATAA

50

(2) INFORMATION FOR SEQ ID NO:585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human papilloma virus type-16 E6/E7 (start site 97)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:585:

GAACCGAAAC CGGTTAGTAT AAAAGCAGAC ATTTTATGCA CCAAAGAGA

50

(2) INFORMATION FOR SEQ ID NO:586:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Human papilloma virus type-18 E6
(start site 105)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:

GGACCGAAAA CGGTGTATAT AAAAGATGTG AGAAACACAC CACAATACTA

50

(2) INFORMATION FOR SEQ ID NO:587:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Parvovirus h-1 H-1[+.04] (start
site 209)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:

AGTGGGCGTG GCTAACTGTA TATAAGCAGT CACTCTGGTC GGTTACTCAC

50

(2) INFORMATION FOR SEQ ID NO:588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Parvovirus h-1 H-1 [+40] (start site 2010)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

GCCGAAGCTA GACACTCCTA TAAATTCGCT AGGTTCATG CGCTCACCAT

50

(2) INFORMATION FOR SEQ ID NO:589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human parvovirus B19-Au B19 [0.06] (start site 347)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:

GAGCGTAGGC GGGGACTACA GTATATATAG CACGGTACTG CCGCAGCTCT

50

(2) INFORMATION FOR SEQ ID NO:590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Simian virus 40 T/t late (start site 31)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:

CCGCCCCCTAA CTCCGCCAG TTCCGCCAT TCTCCGCCCC ATGGCTGACT

50

(2) INFORMATION FOR SEQ ID NO:591:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Simian virus 40 T/t early P2 (start site 5233)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:

TGGCTGACTA ATTTTTTTTA TTTATGCAGA GGCCGAGGCC GCCTCGGCCT

50

(2) INFORMATION FOR SEQ ID NO:592:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

* (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: BK virus T/t early (start site 99)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:592:

CCTGTGGCCT TTTTTTTTAT AATATATAAG AGGCCGAGGC CGCCTCTGCC

50

(2) INFORMATION FOR SEQ ID NO:593:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Polyoma virus T/t E (start site 156)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

GGCCACCCAA ATTGATATAA TTAAGCCCCA ACCGCCTCTT CCCGCCTCAT

50

(2) INFORMATION FOR SEQ ID NO:594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Simian virus 40 late (start site 325)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:

GTTCTTTCCG CCTCAGAAGG TACCTAACCA AGTTCCTCTT TCAGAGGTTA

50

(2) INFORMATION FOR SEQ ID NO:595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Hepatitis B virus subtype adr4 3.6kb P1 (start 1659)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:

AGTTGGGGGA GGAGATTAGG TTAAAGGTCT TTGTACTAGG AGGCTGTAGG

50

(2) INFORMATION FOR SEQ ID NO:596:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Hepatitis B virus subtype adr4 3.6 kb P2 (start 1690)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:

TGTACTAGGA GGCTGTAGGC ATAAATTGGT CTGTTACCA GCACCATGCA

50

(2) INFORMATION FOR SEQ ID NO:597:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Hepatitis B virus subtype adr4 2.2
kb P1 (start 3061)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:

ATCGGCAGTC AGGAAGACAG CCTACTCCCA TCTCTCCACC TCTAAGAGAC

50

(2) INFORMATION FOR SEQ ID NO:598:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Hepatitis B virus subtype adr4 2.2
kb P2 (start 3092)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:

CTCTCCACCT CTAAGAGACA GTCATCCTCA GGCCATGCAG TGGAATCCA

50

(2) INFORMATION FOR SEQ ID NO:599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Epstein Barr virus [BamH1-F] R1
(start 58862)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:

TATTTTGGAA AAGGGATATT ATAAAACAGG TCATTGCTCG GATTGTGGCA

50

(2) INFORMATION FOR SEQ ID NO:600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Promoter Sequence of IL-13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:

GGTGTGAGGC GTCACCACTT GGGCCTATAA AAGCTGCCAC AAGACGCCAA GGCCAC

56

(2) INFORMATION FOR SEQ ID NO:601:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: UL9 BINDING SITE, HSV oriS, higher
affinity

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:

CGTTCGCACT T

11

(2) INFORMATION FOR SEQ ID NO:602:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: UL9 BINDING SITE, HSV oriS, lower affinity

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:

TGCTCGCACT T

11

(2) INFORMATION FOR SEQ ID NO:603:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: UL9Z1 TEST SEQ. / UL9 ASSAY SEQ.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:

GCGCGCGCGC GTTCGCACTT CCGCCGCCGG

30

(2) INFORMATION FOR SEQ ID NO:604:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: UL9Z2 TEST SEQ. / UL9 ASSAY SEQ.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:

GGCGCCGGCC GTTCGCACTT CGCGCGCGCG

30

(2) INFORMATION FOR SEQ ID NO:605:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: UL9 CCCG TEST SEQ. / UL9 ASSAY
SEQ.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:

GGCCCGCCCC GTTCGCACTT CCCGCCCCCG

30

(2) INFORMATION FOR SEQ ID NO:606:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: UL9 GGC TEST SEQ. / UL9 ASSAY
SEQ.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:

GGCGGGCGCC GTTCGCACTT GGGCGGGCGG

30

(2) INFORMATION FOR SEQ ID NO:607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: UL9 ATAT TEST SEQ. / UL9 ASSAY SEQ.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:

GGATATATAC GTTCGCACTT TAATTATTGG

30

(2) INFORMATION FOR SEQ ID NO:608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: UL9 polyA TEST SEQ. / UL9 ASSAY SEQ.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:

GGAAAAAAAC GTTCGCACTT AAAAAAAGG

30

(2) INFORMATION FOR SEQ ID NO:609:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: UL9 polyT TEST SEQ. / UL9 ASSAY

SEQ.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:

GGTTTTTTTC GTTCGCACTT TTTTTTTTGG

30

(2) INFORMATION FOR SEQ ID NO:610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: UL9 GCAC TEST SEQ. / UL9 ASSAY SEQ.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

GGACGCACGC GTTCGCACTT GCAGCAGCGG

30

(2) INFORMATION FOR SEQ ID NO:611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: UL9 ATori-1 Test sequence / UL9 ASSAY SEQ.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:

CGGTATATAT CGTTCGCACT TCGTCCCAAT

30

(2) INFORMATION FOR SEQ ID NO:612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: oriECO2 TEST SEQ. / UL9 ASSAY SEQ.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:

GGCGAATTCG ACGTTCGCAC TTCGTCCCAA T

31

(2) INFORMATION FOR SEQ ID NO:613:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: oriECO3 TEST SEQ. / UL9 ASSAY SEQ.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:

GGCGAATTCG ATCGTTCGCA CTTCGTCCCA AT

32

(2) INFORMATION FOR SEQ ID NO:614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: WILD TYPE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

AAGTGAGAAT TCGAAGCGTT CGCACTTCGT CCCAAT

36

(2) INFORMATION FOR SEQ ID NO:615:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: TRUNCATED UL9 BINDING SITE, COMPARE
SEQ ID NO:601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

TTCGCACTT

9

(2) INFORMATION FOR SEQ ID NO:616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: HSVB1/4, SEQUENCE OF COMPETITOR DNA
MOLECULE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

GGTCGTTTCGC ACTTCGC

17

(2) INFORMATION FOR SEQ ID NO:617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Figure 14B, top strand of an exemplary target sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617:

GCGTANNNNN CGTTCGCACT TNNNNCTTCG TCCCAAT

37

(2) INFORMATION FOR SEQ ID NO:618:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HSV primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:618:

ATTGGGACGA AG

12

(2) INFORMATION FOR SEQ ID NO:619:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: a sample distamycin target sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:

TTCCTCCTTT C

11

(2) INFORMATION FOR SEQ ID NO:620:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: a distamycin target sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:620:

TTCCNNNTTT C

11

(2) INFORMATION FOR SEQ ID NO:621:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Figure 27A, test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:621:

GCGTANNNNN CGTTCGCACT TNNNNCTTCG TCCCAAT

37

(2) INFORMATION FOR SEQ ID NO:622:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Figure 27B, oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:622:

GCGTANNNNN CGTTCGCACT TNNNNCTTCG TCCCAAT

37

(2) INFORMATION FOR SEQ ID NO:623:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Figure 27C, oligonucleotide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:

GCGTANNNNN AAGTGCGAAC GNNNNCTTCG TCCCAAT

37

(2) INFORMATION FOR SEQ ID NO:624:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Figure 27D, oligonucleotide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:

GCGTANNNNN AAGTGCGAAC GNNNNCTTCG TCCCAAT

37

(2) INFORMATION FOR SEQ ID NO:625:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: -35 region consensus sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:

TTGACA

6

(2) INFORMATION FOR SEQ ID NO:626:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: -10 region consensus sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:626:

TATAAT

6

(2) INFORMATION FOR SEQ ID NO:627:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HIV-1, LTR sequence, Figure 28

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:

GTTAGAGTGG AGGTTTGACA GCCGCCTAGC ATTTTCATCAC ATGGCCCGAG AGCTGCATCC 60

GGAGTACTTC AAGAACTGCT GACATCGAGC TTGCTACAAG GGACTTTCCG CTGGGGACTT 120

TCCAGGGAGG CGTGGCCTGG GCGGGACTGG GGAGTGGCGA GCCCTCAGAT CCTGCATATA 180

AGCAGCTGCT TTTTGCCTGT ACTGGGTCTC TCTGGTTAGA CCAGATCTGA GCCTGGGAGC 240

TC 242

(2) INFORMATION FOR SEQ ID NO:628:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: a TFIID binding site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:628:

CCTGCATA

8

(2) INFORMATION FOR SEQ ID NO:629:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: a TFIID binding site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:629:

AAGCAGCT

8

(2) INFORMATION FOR SEQ ID NO:630:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Oligonucleotide, Figure 29A

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:

GCAGAATTCT GCAG

14

(2) INFORMATION FOR SEQ ID NO:631:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Oligonucleotide, Figure 29A

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:

GCAGAATTCT GCAGCGTTCG CACTTTCTAG AGCTCAGG

38

(2) INFORMATION FOR SEQ ID NO:632:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Oligonucleotide, Figure 29A

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:

AGATCTCGAG TCC

13

(2) INFORMATION FOR SEQ ID NO:633:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Oligonucleotide, Figure 29B

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:

GCAGAATTCT GCAGNNNNCG TTCGCACTTT CTAGAGCTCA GG

42

38
13
42

(2) INFORMATION FOR SEQ ID NO:634:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Oligonucleotide, Figure 29C

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:

GCAGAATTCT GCAGNNNNNN NNCGTTGCA CTTTCTAGAG CTCAGG

46

(2) INFORMATION FOR SEQ ID NO:635:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Oligonucleotide, Figure 29D

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:635:

GCAGAATTCT GCAGCGTTG CACTTNNNNN NNNTCTAGAG CTCAGG

46

(2) INFORMATION FOR SEQ ID NO:636:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Oligonucleotide, Figure 30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:636:

CGTGAATTCT GCAG

14

(2) INFORMATION FOR SEQ ID NO:637:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Oligonucleotide, Figure 30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637:

CGTGAATTCT GCAGATG

17

(2) INFORMATION FOR SEQ ID NO:638:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Oligonucleotide, Figure 30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:638:

CGTGAATTCT GCAGATGAGG TACCNNNNNN CGTTCGCACT TTCTAGAGCT CTCC

54

(2) INFORMATION FOR SEQ ID NO:639:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Oligonucleotide, Figure 30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:639:

GTGAAAGATC TCGAGAGG

18

(2) INFORMATION FOR SEQ ID NO:640:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Oligonucleotide, Figure 30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:640:

AAGATCTCGA GAGG

14

(2) INFORMATION FOR SEQ ID NO:641:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: UL9 BINDING SITE, HSV oris

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641:

CGTTCTCACT T

11

(2) INFORMATION FOR SEQ ID NO:642:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Trimeric test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:642:

ACGTACGTAC GT

12

(2) INFORMATION FOR SEQ ID NO:643:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Figure 12 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:643:

AGCTTTCGCA CTTAGCT

17.

(2) INFORMATION FOR SEQ ID NO:644:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Figure 12 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:644:

AGCATTCGCA CTTAGCA

17

(2) INFORMATION FOR SEQ ID NO:645:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Figure 12 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:645:

AGCCTTCGCA CTTAGCC

17

(2) INFORMATION FOR SEQ ID NO:646:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Figure 12 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:646:

AGCGTTCGCA CTTAGCG

17

(2) INFORMATION FOR SEQ ID NO:647:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Figure 12 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:647:

TGCTTTCGCA CTTTGCT

17

(2) INFORMATION FOR SEQ ID NO:648:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Figure 12 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:648:

TGCATTCGCA CTTTGCA

17

(2) INFORMATION FOR SEQ ID NO:649:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Figure 12 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:649:

TGCCTTCGCA CTTTGCC

17

(2) INFORMATION FOR SEQ ID NO:650:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Figure 12 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:650:

TGCGTTCGCA CTTTGCG

17

(2) INFORMATION FOR SEQ ID NO:651:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Figure 12 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:651:

CCATTTCGCA CTTCCAT

17

(2) INFORMATION FOR SEQ ID NO:652:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Figure 12 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:652:

CCCTTTTCGCA CTTCCCT

17

(2) INFORMATION FOR SEQ ID NO:653:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Figure 12 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:653:

CCGTTTCGCA CTTCCGT

17

(2) INFORMATION FOR SEQ ID NO:654:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Figure 12 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:654:

CCTTTTCGCA CTTCCCT

17

(2) INFORMATION FOR SEQ ID NO:655:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Figure 26 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:655:

TTCCNNTTCC

9

(2) INFORMATION FOR SEQ ID NO:656:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Figure 26 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:656:

TTCCNNTTCC

10

(2) INFORMATION FOR SEQ ID NO:657:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Figure 26 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657:

TTCCNNNTTC C

11

(2) INFORMATION FOR SEQ ID NO:658:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Figure 26 test oligonucleotide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:658:

TTCCNNNNNTT CC

12

(2) INFORMATION FOR SEQ ID NO:659:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Figure 31 test oligonucleotide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:659:

CGTTCGCACT TTTAC

15

(2) INFORMATION FOR SEQ ID NO:660:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Figure 31 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:660:

CGTTCGCACT TTACN

15

(2) INFORMATION FOR SEQ ID NO:661:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Figure 31 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:661:

CGTTCGCACT TACNN

15

(2) INFORMATION FOR SEQ ID NO:662:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Figure 32 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:662:

CCCGGGTTAC

10

(2) INFORMATION FOR SEQ ID NO:663:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Figure 32 test oligonucleotide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:663:

CCCGGGTACN

10

(2) INFORMATION FOR SEQ ID NO:664:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Figure 32 test oligonucleotide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:664:

CCCGGGACNN

10